

GenCore version 5.1.7  
 Copyright (c) 1993 - 2006 Bioceleration Ltd.  
 OM protein - protein search, using sw model  
 Run on: February 8, 2006, 16:54:56 ; Search time 118.5 Seconds  
 (without alignments)  
 1019.010 Million cell updates/sec  
 Title: US-10-600-997-6  
 Perfect score: 1552  
 Sequence: 1 MKTLPAMLTGKLFVWFFLI.....RLARNVKEAPTEYASICVRS 289  
 Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5  
 Searched: 1867569 seqs, 417829326 residues  
 Total number of hits satisfying chosen parameters: 1867569  
 Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000  
 Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Published Applications\_AA\_Main:  
 1: /cgn2\_6/prodata/1/pubpaa/US07\_PUBCOMB.pap:  
 2: /cgn2\_6/prodata/1/pubpaa/US08\_PUBCOMB.pap:  
 3: /cgn2\_6/prodata/1/pubpaa/US09\_PUBCOMB.pap:  
 4: /cgn2\_6/prodata/1/pubpaa/US10A\_PUBCOMB.pap:  
 5: /cgn2\_6/prodata/1/pubpaa/US10B\_PUBCOMB.pap:  
 6: /cgn2\_6/prodata/1/pubpaa/US11\_PUBCOMB.pap:  
 Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1552	100.0	289	4	US-10-371-341-2
2	1552	100.0	289	4	US-10-600-997-6
3	1552	100.0	289	5	US-10-831-622-21
4	1552	100.0	289	5	US-10-964-215-21
5	1552	100.0	289	5	US-10-989-826-28
6	1552	100.0	521	5	US-10-831-622-98
7	1552	100.0	521	5	US-10-964-215-98
8	1516	97.7	289	4	US-10-600-997-8
9	1383	89.1	259	5	US-10-831-622-20
10	1383	89.1	259	5	US-10-964-215-20
11	1282	82.6	239	5	US-10-831-622-19
12	1282	82.6	239	5	US-10-964-215-19
13	1256	80.9	241	4	US-10-471-449-10
14	980	63.1	178	5	US-10-831-622-15
15	980	63.1	178	5	US-10-964-215-15
16	860	55.4	157	5	US-10-831-622-13
17	860	55.4	157	5	US-10-964-215-13
18	811	52.3	148	5	US-10-831-622-14
19	811	52.3	148	5	US-10-964-215-14
20	745.5	48.0	212	4	US-10-062-548-88
21	745.5	48.0	212	5	US-10-918-446-88
22	745.5	48.0	212	6	US-11-002-755-88
23	745.5	48.0	212	6	US-11-002-756-88
24	743.5	47.9	306	4	US-10-600-997-5
25	743.5	47.9	306	4	US-10-600-997-10
26	739.5	47.6	306	5	US-10-831-622-63
27	739.5	47.6	306	5	US-10-964-215-63

28	739.5	47.6	538	5	US-10-831-622-99	Sequence 99, Appl
29	739.5	47.6	538	5	US-10-964-215-99	Sequence 99, Appl
30	692	44.6	132	5	US-10-831-622-18	Sequence 18, Appl
31	692	44.6	132	5	US-10-964-215-18	Sequence 18, Appl
32	691	44.5	127	5	US-10-831-622-12	Sequence 12, Appl
33	691	44.5	127	5	US-10-964-215-12	Sequence 12, Appl
34	673.5	43.4	277	5	US-10-831-622-62	Sequence 62, Appl
35	673.5	43.4	277	5	US-10-964-215-62	Sequence 62, Appl
36	635.5	40.9	250	5	US-10-831-622-61	Sequence 61, Appl
37	635.5	40.9	250	5	US-10-964-215-61	Sequence 61, Appl
38	572	36.9	111	5	US-10-831-622-17	Sequence 17, Appl
39	572	36.9	111	5	US-10-964-215-17	Sequence 17, Appl
40	516	33.2	102	4	US-10-062-548-107	Sequence 107, App
41	516	33.2	102	5	US-10-918-446-107	Sequence 107, App
42	516	33.2	102	6	US-11-002-755-107	Sequence 107, App
43	516	33.2	102	6	US-11-002-756-107	Sequence 107, App
44	474	30.5	204	5	US-10-831-622-57	Sequence 57, Appl
45	474	30.5	204	5	US-10-964-215-57	Sequence 57, Appl

ALIGNMENTS

RESULT 1  
 US-10-371-341-2  
 ; Sequence 2, Application US/10371341  
 ; Publication No. US20040091884A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HILARY CLARK  
 ; APPLICANT: DANIEL L. EATON  
 ; APPLICANT: AUSTIN L. GURNEY  
 ; APPLICANT: BERND WRANIK  
 ; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR THE TREATMENT OF  
 ; TITLE OF INVENTION: IMMUNE RELATED DISEASES  
 ; FILE REFERENCE: P1996R1-US  
 ; CURRENT APPLICATION NUMBER: US/10/371,341  
 ; PRIOR FILING DATE: 2003-02-19  
 ; PRIOR APPLICATION NUMBER: US 60/421,236  
 ; PRIOR FILING DATE: 2002-10-25  
 ; NUMBER OF SEQ ID NOS: 2  
 ; SEQ ID NO 2  
 ; LENGTH: 289  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapien  
 US-10-371-341-2

Query Match		100.0%	Score 1552;	DB 4;	Length 289;
Best Local Similarity		100.0%	Pred. No. 1.5e-146;		
Matches 289;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MKTLPAMLTGKLFVWFFLI	PYLDIWNTHGKESCDVLYIKROSEHSILAGDPFLECPV	60	
Db	1	MKTLPAMLTGKLFVWFFLI	PYLDIWNTHGKESCDVLYIKROSEHSILAGDPFLECPV	60	
Qy	61	KYCANRPHVTWCKLNGTTCVKLEDRQTSWKBEKNISFFILHPEPVL	PNDNGSYRCSANFQ	120	
Db	61	KYCANRPHVTWCKLNGTTCVKLEDRQTSWKBEKNISFFILHPEPVL	PNDNGSYRCSANFQ	120	
Qy	121	SNLISHSTTLVYVDVKASERPSKDEMASRPWLLYSLLPLGGLPLLI	TCFLFCCLLR	180	
Db	121	SNLISHSTTLVYVDVKASERPSKDEMASRPWLLYSLLPLGGLPLLI	TCFLFCCLLR	180	
Qy	181	HOGKONELSDTAGREINLVDAHLKSEOTEASTRONSOVLSETGYLDNDP	DLCPFRMDEGS	240	
Db	181	HOGKONELSDTAGREINLVDAHLKSEOTEASTRONSOVLSETGYLDNDP	DLCPFRMDEGS	240	
Qy	241	EYVSNPCLEENKPGIVYASLNHSVIGLNSRLARNVKEAPTEYASICVRS	289		
Db	241	EYVSNPCLEENKPGIVYASLNHSVIGLNSRLARNVKEAPTEYASICVRS	289		

RESULT 2  
 US-10-600-997-6

```

; Sequence 6, Application US/10600997
; Publication No. US20040175380A1
; GENERAL INFORMATION:
; APPLICANT: Allison, James
; APPLICANT: Murphy, Kenneth
; APPLICANT: Watanabe, Norihiko
; APPLICANT: Murphy, Theresa
; APPLICANT: Yang, Jianfei
; APPLICANT: Zang, Xingxing
; TITLE OF INVENTION: Compositions and Methods for Modulating Lymphocyte Activity
; FILE REFERENCE: A-71608/TAL/DRH
; CURRENT APPLICATION NUMBER: US/10/600,997
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 60/390,653
; PRIOR FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: US 60/438,593
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 6
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-600-997-6

```

```

Query Match      100.0%; Score 1552; DB 4; Length 289;
Best Local Similarity 100.0%; Pred. No. 1.5e-146;
Matches 289; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 M K T L P A M L G T G K L F W V F F L I P Y L D I W N I H G K E S C D V Q L Y I K R Q S H S I L A G D P F F L E C P V 60
D b 1 M K T L P A M L G T G K L F W V F F L I P Y L D I W N I H G K E S C D V Q L Y I K R Q S H S I L A G D P F F L E C P V 60

QY 61 K Y C A N R P H V T W C K L N G T T C V K L E D R Q T S W K E E K N I S F F I L H P E P V L P N D N G S Y R C S A N F Q 120
D b 61 K Y C A N R P H V T W C K L N G T T C V K L E D R Q T S W K E E K N I S F F I L H P E P V L P N D N G S Y R C S A N F Q 120

QY 121 S N L I E S H S T T L Y V T D V K S A S E R P S K D E M A S R P W L Y S L L P L G G L P L L I T T C F L C F C C L R R 180
D b 121 S N L I E S H S T T L Y V T D V K S A S E R P S K D E M A S R P W L Y S L L P L G G L P L L I T T C F L C F C C L R R 180

QY 181 H O G K Q N E L S D T A G R E I N L V D A H L K S E Q T E A S T R Q N S Q V L L S E T G I Y D N D P D L C F R M Q E G S 240
D b 181 H O G K Q N E L S D T A G R E I N L V D A H L K S E Q T E A S T R Q N S Q V L L S E T G I Y D N D P D L C F R M Q E G S 240

QY 241 E V Y S N P C L E E N K P G I V Y A S L N H S V I G L N S R L A R N V K E A P T E Y A S I C V R S 289
D b 241 E V Y S N P C L E E N K P G I V Y A S L N H S V I G L N S R L A R N V K E A P T E Y A S I C V R S 289

```

```

RESULT 3
US-10-831-622-21
; Sequence 21, Application US/10831622
; Publication No. US20040248257A1
; GENERAL INFORMATION:
; APPLICANT: Kaye, Jonathan
; APPLICANT: Wilkinson, Beverley
; TITLE OF INVENTION: SPEX COMPOSITIONS AND METHODS OF USE
; FILE REFERENCE: TSRI 810.1
; CURRENT APPLICATION NUMBER: US/10/831,622
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/467,206
; PRIOR FILING DATE: 2003-04-30
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-831-622-21

```

```

Query Match      100.0%; Score 1552; DB 5; Length 289;
Best Local Similarity 100.0%; Pred. No. 1.5e-146;

```

```

Matches 289; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 M K T L P A M L G T G K L F W V F F L I P Y L D I W N I H G K E S C D V Q L Y I K R Q S H S I L A G D P F F L E C P V 60
D b 1 M K T L P A M L G T G K L F W V F F L I P Y L D I W N I H G K E S C D V Q L Y I K R Q S H S I L A G D P F F L E C P V 60

QY 61 K Y C A N R P H V T W C K L N G T T C V K L E D R Q T S W K E E K N I S F F I L H P E P V L P N D N G S Y R C S A N F Q 120
D b 61 K Y C A N R P H V T W C K L N G T T C V K L E D R Q T S W K E E K N I S F F I L H P E P V L P N D N G S Y R C S A N F Q 120

QY 121 S N L I E S H S T T L Y V T D V K S A S E R P S K D E M A S R P W L Y S L L P L G G L P L L I T T C F L C F C C L R R 180
D b 121 S N L I E S H S T T L Y V T D V K S A S E R P S K D E M A S R P W L Y S L L P L G G L P L L I T T C F L C F C C L R R 180

QY 181 H O G K Q N E L S D T A G R E I N L V D A H L K S E Q T E A S T R Q N S Q V L L S E T G I Y D N D P D L C F R M Q E G S 240
D b 181 H O G K Q N E L S D T A G R E I N L V D A H L K S E Q T E A S T R Q N S Q V L L S E T G I Y D N D P D L C F R M Q E G S 240

QY 241 E V Y S N P C L E E N K P G I V Y A S L N H S V I G L N S R L A R N V K E A P T E Y A S I C V R S 289
D b 241 E V Y S N P C L E E N K P G I V Y A S L N H S V I G L N S R L A R N V K E A P T E Y A S I C V R S 289

```

```

RESULT 4
US-10-964-215-21
; Sequence 21, Application US/10964215
; Publication No. US20050152893A1
; GENERAL INFORMATION:
; APPLICANT: Kaye, Jonathan
; TITLE OF INVENTION: METHODS AND MATERIALS FOR THE INHIBITION
; FILE REFERENCE: TSRI 810.2
; CURRENT APPLICATION NUMBER: US/10/964,215
; CURRENT FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: US 10/831,622
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/467,206
; PRIOR FILING DATE: 2003-04-30
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-964-215-21

```

```

Query Match      100.0%; Score 1552; DB 5; Length 289;
Best Local Similarity 100.0%; Pred. No. 1.5e-146;
Matches 289; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 M K T L P A M L G T G K L F W V F F L I P Y L D I W N I H G K E S C D V Q L Y I K R Q S H S I L A G D P F F L E C P V 60
D b 1 M K T L P A M L G T G K L F W V F F L I P Y L D I W N I H G K E S C D V Q L Y I K R Q S H S I L A G D P F F L E C P V 60

QY 61 K Y C A N R P H V T W C K L N G T T C V K L E D R Q T S W K E E K N I S F F I L H P E P V L P N D N G S Y R C S A N F Q 120
D b 61 K Y C A N R P H V T W C K L N G T T C V K L E D R Q T S W K E E K N I S F F I L H P E P V L P N D N G S Y R C S A N F Q 120

QY 121 S N L I E S H S T T L Y V T D V K S A S E R P S K D E M A S R P W L Y S L L P L G G L P L L I T T C F L C F C C L R R 180
D b 121 S N L I E S H S T T L Y V T D V K S A S E R P S K D E M A S R P W L Y S L L P L G G L P L L I T T C F L C F C C L R R 180

QY 181 H O G K Q N E L S D T A G R E I N L V D A H L K S E Q T E A S T R Q N S Q V L L S E T G I Y D N D P D L C F R M Q E G S 240
D b 181 H O G K Q N E L S D T A G R E I N L V D A H L K S E Q T E A S T R Q N S Q V L L S E T G I Y D N D P D L C F R M Q E G S 240

QY 241 E V Y S N P C L E E N K P G I V Y A S L N H S V I G L N S R L A R N V K E A P T E Y A S I C V R S 289
D b 241 E V Y S N P C L E E N K P G I V Y A S L N H S V I G L N S R L A R N V K E A P T E Y A S I C V R S 289

```

```

RESULT 5
US-10-989-826-28

```

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 8, 2006, 16:43:11 ; Search time 143 Seconds  
(without alignments)  
887.975 Million cell updates/sec

Title: US-10-600-997-6  
Perfect score: 1552  
Sequence: 1 MKTLPMLGTGKLFVFFLI.....RLARNVKEAPTEVASYICVRS 289

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_21.\*

- 1: Geneseq1980s.\*
- 2: Geneseq1990s.\*
- 3: Geneseq2000s.\*
- 4: Geneseq2001s.\*
- 5: Geneseq2002s.\*
- 6: Geneseq2003as.\*
- 7: Geneseq2003bs.\*
- 8: Geneseq2004s.\*
- 9: Geneseq2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1552	100.0	289	8 ADH34661	Adh34661 Human BTL
2	1552	100.0	289	8 ADO43716	Ado43716 Amino aci
3	1552	100.0	289	8 ADUS1070	Adus1070 Human spl
4	1552	100.0	289	8 ADV34145	Adv34145 Human BTL
5	1552	100.0	289	9 AEA23330	Aea23330 Tumor ant
6	1552	100.0	521	8 ADUS1147	Adus1147 Spleen-ex
7	1545	99.5	289	8 ADH74500	Adh74500 Human mcd
8	1516	97.7	289	8 ADH34662	Adh34662 Human BTL
9	1515	97.6	283	8 ADH74498	Adh74498 Human mcd
10	1383	89.1	259	8 ADUS1069	Adus1069 Human spl
11	1282	82.6	239	8 ADUS1068	Adus1068 Human SPE
12	1256	80.9	241	5 ABG96272	Abg96272 Human imm
13	1256	80.9	241	8 ADV34146	Adv34146 Sequence
14	998	64.3	194	9 ADY19218	Ady19218 PRO polyp
15	980	63.1	178	8 ADUS1064	Adus1064 Human SPE
16	860	55.4	157	8 ADUS1062	Adus1062 Human SPE
17	830	53.5	390	8 ADV34147	Adv34147 Surface I
18	811	52.3	148	8 ADUS1063	Adus1063 Human SPE
19	745.5	48.0	212	2 AAY30839	Aay30839 Human sec
20	745.5	48.0	212	6 ADA57288	Ada57288 Human sec
21	745.5	48.0	212	6 ADA41169	Ada41169 Human sec
22	743.5	47.9	306	8 ADH34664	Adh34664 Mouse BTL
23	739.5	47.6	306	8 ADUS1112	Adus1112 Murine sp
24	739.5	47.6	538	8 ADUS1148	Adus1148 Spleen-ex

25	692	44.6	132	8 ADUS1067	Adus1067 Human SPE
26	691	44.5	127	8 ADUS1061	Adus1061 Human SPE
27	673.5	43.4	277	8 ADUS1111	Adus1111 Murine sp
28	635.5	40.9	250	8 ADUS1110	Adus1110 Murine SP
29	572	36.9	111	8 ADUS1066	Adus1066 Human spl
30	536	34.5	98	9 AEB92075	Aeb92075 Human BTL
31	516	33.2	101	6 ADA57590	Ada57590 Human sec
32	516	33.2	101	6 ADA41487	Ada41487 Human sec
33	516	33.2	102	2 AAY30859	Aay30859 Human sec
34	474	30.5	204	8 ADUS1106	Adus1106 Murine SP
35	440	28.4	78	3 AAG02951	Aag02951 Human sec
36	408	26.3	175	8 ADUS1105	Adus1105 Murine SP
37	408	26.3	179	8 ADUS1134	Adus1134 Murine SP
38	408	26.3	411	8 ADUS1149	Adus1149 Spleen-ex
39	398.5	25.7	180	8 ADUS1104	Adus1104 Murine SP
40	377	24.3	65	8 ADUS1052	Adus1052 Human spl
41	355	22.9	67	8 ADUS1055	Adus1055 Human SPE
42	342	22.0	150	8 ADUS1135	Adus1135 Murine SP
43	341	22.0	126	8 ADUS1109	Adus1109 Murine SP
44	332.5	21.4	151	8 ADUS1103	Adus1103 Murine SP
45	265.5	17.1	102	8 ADUS1108	Adus1108 Murine sp

## ALIGNMENTS

RESULT 1

ADH34661

ID ADH34661 standard; protein; 289 AA.

XX ADH34661;

XX 11-MAR-2004 (first entry)

XX Human BTLA.

XX B7x; ligand; B and T lymphocyte attenuator; BTLA; tumour; inhibition;

XX tumour-specific; immunological tolerance; cancer; autoimmune disease;  
 XX diabetes; pre-eclampsia; rheumatoid arthritis; multiple sclerosis;  
 XX infection; graft rejection; cell cycle progression; differentiation;  
 XX survival; cytokine production; cytolytic activation;  
 XX antigen presentation; antibody production.  
 XX Homo sapiens.

Key	Location/Qualifiers
Peptide	1..28
Disulfide-bond	/note= "Signal peptide"
Modified-site	/note = Disulphide bond
Domain	/note= "Glycosylated"
Region	154..182
Region	223..229
Region	/note= "Conserved sequence"
Region	254..262
Region	/note= "Conserved sequence"
Region	277..289
Region	/note= "Conserved sequence"

WO2004000221-A2.

31-DEC-2003.

20-JUN-2003; 2003WO-US019614.

20-JUN-2002; 2002US-0390653P.

06-JAN-2003; 2003US-0438593P.

(REGC ) UNIV CALIFORNIA.

(UNIW ) UNIV WASHINGTON.

PI Allison JP, Murphy KP, Watanabe N, Murphy TL, Yang J, Zang X;  
 XX WPI; 2004-082409/08.  
 XX  
 PT New recombinant B and T lymphocyte attenuator nucleic acid and protein,  
 PT useful for modulating B and T lymphocyte activity, or for diagnosing and  
 PT treating cancer, autoimmune disease or infectious disease.  
 XX  
 XX Example 4; Fig 19; 11pp; English.  
 XX  
 CC This sequence represents a human B and T lymphocyte attenuator (BTLA).  
 CC BTLA acts as a negative regulator of both B and T lymphocyte activity,  
 CC where signaling mediated by BTLA results in the inhibition of BTLA-  
 CC positive lymphocyte activity. In BTLA-positive T cells BTLA signalling  
 CC can inhibit TCR-induced T cell responses, such as cell cycle progression,  
 CC differentiation, survival, cytokine production and cytolytic activation.  
 CC In BTLA-positive B cells BTLA signalling can inhibit B cell antigen  
 CC receptor-induced B cell responses, such as cell cycle progression,  
 CC differentiation, survival, antigen presentation and antibody production.  
 CC B7x is a ligand for the recombinant BTLA of the invention. B7x is able to  
 CC negatively regulate B and T lymphocyte activity through its interaction  
 CC with BTLA, which inhibits both B and T cell responses. Therefore B7x  
 CC positive tumour tissue inhibits the activity of tumour-specific T cells.  
 CC B7x is also expressed on non-tumour non-lymphoid tissue, showing that the  
 CC B7x/BTLA interaction is a mechanism for maintaining immunological  
 CC tolerance. BTLA proteins and related nucleic acids are useful for  
 CC modulating B and T lymphocyte activity, for diagnosing and treating  
 CC cancer, autoimmune disease, e.g. diabetes, pre-eclampsia, rheumatoid  
 CC arthritis or multiple sclerosis, or infectious disease, or for preventing  
 CC acute and/or chronic graft rejection.  
 XX  
 SQ Sequence 289 AA;

Query Match 100.0%; Score 1552; DB 8; Length 289;  
 Best Local Similarity 100.0%; Pred. No. 8.1e-139;  
 Matches 289; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MKTLPAMLTGKLFVFFFLIPYLDIWNTHGKSCDQVLYIKRQSEHSILAGDPFELECPV 60  
 DB 1 MKTLPAMLTGKLFVFFFLIPYLDIWNTHGKSCDQVLYIKRQSEHSILAGDPFELECPV 60  
 QY 61 KYCANRPHVTWCKLNGTTCVKLEDROTQSWKEKNISFFILHPEPVLNDNGSYRCSANFQ 120  
 DB 61 KYCANRPHVTWCKLNGTTCVKLEDROTQSWKEKNISFFILHPEPVLNDNGSYRCSANFQ 120  
 QY 121 SNLIESHSSTLVYTDVKSASRPSKDEMASRPWLLYSLLPLGGLPLLIITTCFLCFLRR 180  
 DB 121 SNLIESHSSTLVYTDVKSASRPSKDEMASRPWLLYSLLPLGGLPLLIITTCFLCFLRR 180  
 QY 181 HQGKQNELSDTAGREINLVDAHLKSEOTEASTRONSQVLLSETGIYDNDPDLCFRMOEGS 240  
 DB 181 HQGKQNELSDTAGREINLVDAHLKSEOTEASTRONSQVLLSETGIYDNDPDLCFRMOEGS 240  
 QY 241 EYVSNPCLNEKPGIYVINSVIGLSNRLARNVKEAPTEYASICVRS 289  
 DB 241 EYVSNPCLNEKPGIYVINSVIGLSNRLARNVKEAPTEYASICVRS 289

RESULT 2  
 ADO43716  
 ID ADO43716 standard; protein; 289 AA.  
 XX  
 AC ADO43716;  
 XX  
 XX 29-JUL-2004 (first entry)  
 XX  
 XX Amino acid sequence of PRO87299.  
 XX human; PRO87299; gene therapy; tumour; immune related disease.  
 XX Homo sapiens.  
 XX  
 XX Key Location/Qualifiers

FT Modified-site 31. .39 /note="tyrosine kinase phosphorylation site"  
 FT Modified-site 41. .44 /note="CAMP- and cGMP-dependent protein kinase  
 FT phosphorylation site"  
 FT Domain 51. .117 /note = immunoglobulin domain  
 FT Modified-site 75. .78 /note= "N-glycosylation site"  
 FT Modified-site 94. .97 /note= "N-glycosylation site"  
 FT Modified-site 110. .113 /note= "N-glycosylation site"  
 FT Modified-site 111. .116 /note= "N-glycosylation site"  
 FT Domain 153. .173 /note= "N-myristoylation site"  
 FT Modified-site 224. .229 /note = transmembrane domain  
 FT Modified-site 254. .259 /note= "N-myristoylation site"  
 FT Domain 255. .260 /note = ITIM domain  
 FT Modified-site 261. .264 /note= "N-glycosylation site"  
 FT Domain 280. .285 /note = ITISM domain  
 PN WO2004039394-A1.  
 XX 13-MAY-2004.  
 XX  
 PF 19-FEB-2003; 2003WO-US005335.  
 PR 25-OCT-2002; 2002US-0421236P.  
 XX (GETH ) GENENTECH INC.  
 PA Clark H, Eaton DL, Gurney AL, Wranik B;  
 PI WPI; 2004-376066/35.  
 DR N-PSDB; ADO43715.  
 XX  
 PT New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO20080 or  
 PT PRO21383, useful in molecular biology, chromosome and gene mapping, in  
 PT generating antisense RNA and DNA, and in gene therapy.  
 XX  
 PS Claim 9; Fig 2; 98pp; English.  
 XX  
 CC The present sequence represents a human polypeptide designated PRO87299.  
 CC The polynucleotide is useful in molecular biology, including uses as  
 CC hybridization probes, in chromosome and gene mapping, in generating  
 CC antisense RNA and DNA, and in gene therapy. The polynucleotide may also  
 CC be used in preparing PRO polypeptides by recombinant techniques, and in  
 CC generating either transgenic animals or knock-out animals which, in turn,  
 CC are useful in the development and screening of therapeutically useful  
 CC reagents. The PRO polypeptide is used in preparing a medicament for  
 CC treating a condition responsive to the polypeptide, such as tumours and  
 CC immune related diseases.  
 XX  
 SQ Sequence 289 AA;

Query Match 100.0%; Score 1552; DB 8; Length 289;  
 Best Local Similarity 100.0%; Pred. No. 8.1e-139;  
 Matches 289; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MKTLPAMLTGKLFVFFFLIPYLDIWNTHGKSCDQVLYIKRQSEHSILAGDPFELECPV 60  
 DB 1 MKTLPAMLTGKLFVFFFLIPYLDIWNTHGKSCDQVLYIKRQSEHSILAGDPFELECPV 60  
 QY 61 KYCANRPHVTWCKLNGTTCVKLEDROTQSWKEKNISFFILHPEPVLNDNGSYRCSANFQ 120  
 DB 61 KYCANRPHVTWCKLNGTTCVKLEDROTQSWKEKNISFFILHPEPVLNDNGSYRCSANFQ 120

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 8, 2006, 16:54:06 ; Search time 34.5 Seconds  
(without alignments)  
692.559 Million cell updates/sec

Title: US-10-600-997-6  
Perfect score: 1552  
Sequence: 1 MKTLPAMLTGKLFVFFLI.....RLARNVKEAPTEYASICVRS 289

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/prodata/1/iaa/5 COMB.pep.\*  
2: /cgn2\_6/prodata/1/iaa/6 COMB.pep.\*  
3: /cgn2\_6/prodata/1/iaa/H COMB.pep.\*  
4: /cgn2\_6/prodata/1/iaa/PCTUS COMB.pep.\*  
5: /cgn2\_6/prodata/1/iaa/RE COMB.pep.\*  
6: /cgn2\_6/prodata/1/iaa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	745.5	48.0	212	2	US-09-369-247-88
2	745.5	48.0	212	2	US-10-062-548-88
3	516	33.2	102	2	US-09-369-247-107
4	516	33.2	102	2	US-10-062-548-107
5	440	28.4	78	2	US-09-513-999C-7032
6	119.5	7.7	343	1	US-08-348-792-10
7	119.5	7.7	343	1	US-08-462-738-10
8	119.5	7.7	343	2	US-09-199-955-10
9	119.5	7.7	343	2	US-08-880-875-10
10	118	7.6	1953	2	US-09-917-254-92
11	113	7.3	624	1	US-08-642-406A-22
12	113	7.3	624	2	US-09-199-534-22
13	113	7.3	624	2	US-09-199-534-22
14	113	7.3	624	2	US-09-491-322-22
15	113	7.3	773	2	US-08-434-000A-2
16	113	7.3	773	2	US-09-312-157-2
17	113	7.3	773	2	US-09-717-888-2
18	113	7.3	773	2	US-09-818-247-6
19	105.5	6.8	278	2	US-09-270-767-42034
20	100.5	6.5	119	2	US-09-858-664A-30
21	100.5	6.5	119	2	US-10-274-978-31
22	100.5	6.5	119	2	US-10-697-263-31
23	100.5	6.5	739	2	US-09-854-845-45
24	100.5	6.5	744	2	US-09-854-845-43
25	100.5	6.5	838	2	US-09-854-845-29
26	100.5	6.5	843	2	US-09-854-845-27
27	99.5	6.4	329	1	US-08-348-792-12

28	99.5	6.4	329	1	US-08-462-738-12	Sequence 12, Appl
29	99.5	6.4	329	2	US-09-199-955-12	Sequence 12, Appl
30	99.5	6.4	329	2	US-08-880-875-12	Sequence 12, Appl
31	96.5	6.2	766	2	US-09-854-845-49	Sequence 49, Appl
32	96.5	6.2	771	2	US-09-854-845-47	Sequence 47, Appl
33	96.5	6.2	865	2	US-09-854-845-33	Sequence 33, Appl
34	96.5	6.2	870	2	US-09-854-845-31	Sequence 31, Appl
35	96	6.2	771	1	US-08-742-753-2	Sequence 2, Appl
36	92.5	6.0	1209	2	US-09-130-158A-2	Sequence 4, Appl
37	91.5	5.9	570	2	US-08-991-944-4	Sequence 21, Appl
38	91.5	5.9	570	2	US-09-173-151A-21	Sequence 2, Appl
39	91.5	5.9	622	2	US-09-499-846-2	Sequence 10, Appl
40	91.5	5.9	731	1	US-08-070-165F-10	Sequence 10, Appl
41	91.5	5.9	731	1	US-08-885-418-10	Sequence 1, Appl
42	90.5	5.8	816	1	US-07-640-029-1	Sequence 7023, Ap
43	89.5	5.8	631	2	US-09-543-681A-7023	Sequence 2, Appl
44	89.5	5.8	4391	2	US-10-006-011A-2	Sequence 6, Appl
45	89	5.7	820	1	US-08-166-717D-6	

## ALIGNMENTS

RESULT 1  
US-09-369-247-88  
; Sequence 88, Application US/09369247  
; Patent No. 6569992  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 44 Human Secreted Proteins  
; FILE REFERENCE: P2024P1  
; CURRENT APPLICATION NUMBER: US/09/369,247  
; CURRENT FILING DATE: 1999-08-05  
; EARLIER APPLICATION NUMBER: 60/074,118  
; EARLIER FILING DATE: 1998-02-09  
; EARLIER APPLICATION NUMBER: 60/074,157  
; EARLIER FILING DATE: 1998-02-09  
; EARLIER APPLICATION NUMBER: 60/074,137  
; EARLIER FILING DATE: 1998-02-09  
; EARLIER APPLICATION NUMBER: 60/074,341  
; EARLIER FILING DATE: 1998-02-09  
; EARLIER APPLICATION NUMBER: 60/074,141  
; EARLIER FILING DATE: 1998-02-09  
; NUMBER OF SEQ ID NOS: 172  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 88  
; LENGTH: 212  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-369-247-88

Query Match 48.0%; Score 745.5; DB 2; Length 212;  
Best Local Similarity 95.1%; Pred. No. 4.6e-70;  
Matches 137; Conservative 3; Mismatches 3; Indels 1; Gaps 1;  
QY 1 MKTLPAMLTGKLFVFFLIPLYLDIWNHKGSCDVLYIKQSEHSILAGDPFLEPCV 60  
Db 1 MKTLPAMLTGKLFVFFLIPLYLDIWNHKGSCDVLYIKQSEHSILAGDPFLEPCV 60  
QY 61 KYCANRPHVTWCKLNGTTCVKLEDRQTSWKBEKNISFFILHPEPVLNDNGSYRCSANFQ 120  
Db 61 KYCANRPHVTWCKLNGTTCVKLEDRQTSWKBEKNISFFILHPEPVLNDNGSYRCSANFQ 120  
QY 121 SNLIESHSTLYVTDVKSASERPS 144  
Db 121 SNLIESHSTLYVTG-EFSTPRPS 143

RESULT 2  
US-10-062-548-88  
; Sequence 88, Application US/10062548  
; Patent No. 6924356  
; GENERAL INFORMATION:

```
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 44 Human Secreted Proteins
; FILE REFERENCE: P2024P1
; CURRENT APPLICATION NUMBER: US/10/062,548
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 09/369,247
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/074,118
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/074,157
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/074,137
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/074,341
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/074,141
; PRIOR FILING DATE: 1998-02-09
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 88
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
; GENERAL INFORMATION:
US-10-062-548-88

Query Match      48.0%; Score 745.5; DB 2; Length 212;
Best Local Similarity 95.1%; Pred. No. 4.6e-70;
Matches 137; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 1 MKTLPAMLTGKLFVWFELIPYLDIWNHKGKSCDVQLYIKRQSEHSILAGDPFEECPV 60
   |||||
Db 1 MKTLPAMLTGKLFVWFELIPYLDIWNHKGKSCDVQLYIKRQSEHSILAGDPFEECPV 60
   |||||

QY 61 KYCANRPHVTWCKLNGTTCVKLEDRQTSWKEEKNIISFFILHFEPLVPNDNGSVRCSANFQ 120
   |||||
Db 61 KYCANRPHVTWCKLNGTTCVKLEDRQTSWKEEKNIISFFILHFEPLVPNDNGSVRCSANFQ 120

QY 121 SNLIESHSTLYVTDVKSASERPS 144
   |||||
Db 121 SNLIESHSTLYVTG-EFSTPRPS 143

RESULT 3
US-09-369-247-107
; Sequence 107, Application US/09369247
; Patent No. 6569992
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 44 Human Secreted Proteins
; FILE REFERENCE: P2024P1
; CURRENT APPLICATION NUMBER: US/09/369,247
; CURRENT FILING DATE: 1999-08-05
; EARLIER APPLICATION NUMBER: 60/074,118
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,157
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,137
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,341
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,141
; EARLIER FILING DATE: 1998-02-09
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 107
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (101)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
```

```
; NAME/KEY: SITE
; LOCATION: (102)
; OTHER INFORMATION: Xaa equals stop translation
US-09-369-247-107

Query Match      33.2%; Score 516; DB 2; Length 102;
Best Local Similarity 93.8%; Pred. No. 2e-46;
Matches 91; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MKTLPAMLTGKLFVWFELIPYLDIWNHKGKSCDVQLYIKRQSEHSILAGDPFEECPV 60
   |||||
Db 1 MKTLPAMLTGKLFVWFELIPYLDIWNHKGKSCDVQLYIKRQSEHSILAGDPFEECPV 60
   |||||

QY 61 KYCANRPHVTWCKLNGTTCVKLEDRQTSWKEEKNIISF 97
   |||||
Db 61 KYCANRPHVTWCKLNGTTCVKLEDRQTSWKKRRTFHF 97

RESULT 4
US-10-062-548-107
; Sequence 107, Application US/10062548
; Patent No. 6924356
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 44 Human Secreted Proteins
; FILE REFERENCE: P2024P1
; CURRENT APPLICATION NUMBER: US/10/062,548
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 09/369,247
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/074,118
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/074,157
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/074,137
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/074,341
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/074,141
; PRIOR FILING DATE: 1998-02-09
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 107
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (101)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
```

```
; NAME/KEY: SITE
; LOCATION: (102)
; OTHER INFORMATION: Xaa equals stop translation
US-10-062-548-107
```

```
Query Match      33.2%; Score 516; DB 2; Length 102;
Best Local Similarity 93.8%; Pred. No. 2e-46;
Matches 91; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MKTLPAMLTGKLFVWFELIPYLDIWNHKGKSCDVQLYIKRQSEHSILAGDPFEECPV 60
   |||||
Db 1 MKTLPAMLTGKLFVWFELIPYLDIWNHKGKSCDVQLYIKRQSEHSILAGDPFEECPV 60
   |||||

QY 61 KYCANRPHVTWCKLNGTTCVKLEDRQTSWKEEKNIISF 97
   |||||
Db 61 KYCANRPHVTWCKLNGTTCVKLEDRQTSWKKRRTFHF 97
```

```
RESULT 5
US-09-513-999C-7032
; Sequence 7032, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
```

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 8, 2006, 16:56:11 ; Search time 10 Seconds  
(without alignments)  
379.241 Million cell updates/sec

Title: US-10-600-997-6

Perfect score: 1552

Sequence: 1 MKTLPAMLTGKLFVFFLI.....RLARNVKEAPTEYSICVRS 289

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 97014 seqs, 1312538 residues

Total number of hits satisfying chosen parameters: 97014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA\_New\*

1: /cgn2\_6/prodata/1/pubpaa/US08\_NEW\_PUB.pbp:\*

2: /cgn2\_6/prodata/1/pubpaa/US06\_NEW\_PUB.pbp:\*

3: /cgn2\_6/prodata/1/pubpaa/US07\_NEW\_PUB.pbp:\*

4: /cgn2\_6/prodata/1/pubpaa/PCT\_NEW\_PUB.pbp:\*

5: /cgn2\_6/prodata/1/pubpaa/US05\_NEW\_PUB.pbp:\*

6: /cgn2\_6/prodata/1/pubpaa/US10\_NEW\_PUB.pbp:\*

7: /cgn2\_6/prodata/1/pubpaa/US11\_NEW\_PUB.pbp:\*

8: /cgn2\_6/prodata/1/pubpaa/US60\_NEW\_PUB.pbp:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1552	100.0	289	6	US-10-987-663-2
2	1539	99.2	295	6	US-10-987-663-10
3	1256	80.9	241	6	US-10-987-663-8
4	90.5	5.8	822	7	US-11-183-567A-2
5	89.5	5.8	3598	6	US-10-995-561-672
6	89.5	5.8	4346	6	US-10-995-561-671
7	89.5	5.8	4347	6	US-10-995-561-670
8	89.5	5.8	4390	7	US-11-169-041-169
9	89.5	5.8	4419	6	US-10-821-234-1155
10	89	5.7	244	7	US-11-156-084-218
11	87	5.6	534	6	US-10-821-234-1341
12	86.5	5.6	976	7	US-11-148-770-31
13	86.5	5.6	1150	7	US-11-139-435-1
14	86.5	5.6	1338	6	US-11-109-156-23
15	85.5	5.5	1338	6	US-10-821-234-1622
16	85.5	5.5	2828	7	US-11-080-991-54
17	85.5	5.5	2828	7	US-11-186-284-49
18	85	5.5	309	6	US-10-453-372-778
19	83.5	5.4	305	6	US-11-000-463-391
20	83.5	5.4	398	6	US-10-821-234-1593
21	83.5	5.4	915	7	US-11-144-987-16
22	83.5	5.4	915	7	US-11-144-987-22
23	83.5	5.4	917	7	US-11-144-987-18
24	83.5	5.4	917	7	US-11-144-987-20
25	83.5	5.4	917	7	US-11-144-987-24

26	83.5	5.4	917	7	US-11-144-987-26	Sequence 26, Appl
27	83	5.3	399	7	US-11-159-919-4	Sequence 4, Appli
28	82.5	5.3	305	7	US-11-000-463-863	Sequence 863, App
29	82.5	5.3	4495	6	US-10-453-372-1002	Sequence 1002, Ap
30	82.5	5.3	5636	7	US-11-065-695-20	Sequence 20, Appl
31	82	5.3	977	7	US-11-093-274-39	Sequence 39, Appl
32	81	5.2	235	6	US-10-453-372-784	Sequence 784, App
33	81	5.2	284	6	US-10-453-372-790	Sequence 790, App
34	81	5.2	290	6	US-10-453-372-776	Sequence 776, App
35	81	5.2	302	6	US-10-453-372-780	Sequence 780, App
36	81	5.2	302	6	US-10-453-372-782	Sequence 782, App
37	81	5.2	302	6	US-10-453-372-788	Sequence 788, App
38	81	5.2	458	6	US-10-453-372-786	Sequence 786, App
39	81	5.2	464	6	US-10-453-372-772	Sequence 772, App
40	81	5.2	464	6	US-10-453-372-774	Sequence 774, App
41	81	5.2	473	6	US-10-453-372-770	Sequence 770, App
42	81	5.2	758	7	US-11-043-693-1	Sequence 1, Appli
43	80	5.2	136	7	US-11-156-084-324	Sequence 324, App
44	80	5.2	900	7	US-11-144-987-4	Sequence 4, Appli
45	80	5.2	902	7	US-11-144-987-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1

US-10-987-663-2

; Sequence 2, Application US/10987663

; Publication No. US20050272118A1

; GENERAL INFORMATION:

; APPLICANT: GENENTECH, INC.

; APPLICANT: CLARK, HILARY

; APPLICANT: EATON, DANIEL L.

; APPLICANT: WRANIK, BERND

; APPLICANT: OUYANG, WENJUN

; APPLICANT: GONZALES, LINO

; APPLICANT: LOYET, KELLY M.

; TITLE OF INVENTION: Novel Compositions and Methods for the Treatment of

; TITLE OF INVENTION: Immune Related Diseases

; FILE REFERENCE: P1996R1P1-US

; CURRENT APPLICATION NUMBER: US/10/987,663

; CURRENT FILING DATE: 2004-11-12

; PRIOR APPLICATION NUMBER: US 60/421,236

; PRIOR FILING DATE: 2002-10-25

; PRIOR APPLICATION NUMBER: US 10/371,341

; PRIOR FILING DATE: 2003-02-19

; NUMBER OF SEQ ID NOS: 10

; SEQ ID NO 2

; LENGTH: 289

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-987-663-2

Query Match 100.0%; Score 1552; DB 6; Length 289;

Best Local Similarity 100.0%; Pred. No. 3e-144;

Matches 289; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKTLPAMLTGKLFVFFLIPLYLDIWNTHGKSCDVLYIKRQSEHSILAGDPFELECPV 60

DB 1 MKTLPAMLTGKLFVFFLIPLYLDIWNTHGKSCDVLYIKRQSEHSILAGDPFELECPV 60

QY 61 KYCANRPHVTTWCKLANGTTCVKLEDQTSWKBEKNISFFILHPEPVLPNONGSVRCSANFQ 120

DB 61 KYCANRPHVTTWCKLANGTTCVKLEDQTSWKBEKNISFFILHPEPVLPNONGSVRCSANFQ 120

QY 121 SNLIESHSITLYVTVDKASERPSKDEMASRPWLLYSLLPLGGLPLIITTCFLCFLCLR 180

DB 121 SNLIESHSITLYVTVDKASERPSKDEMASRPWLLYSLLPLGGLPLIITTCFLCFLCLR 180

QY 181 HOGKQNELSDTAGREINLVDAHLKSEQTEASTRONSQVLLSETGIYDNDPDLCFRMOEGS 240

DB 181 HOGKQNELSDTAGREINLVDAHLKSEQTEASTRONSQVLLSETGIYDNDPDLCFRMOEGS 240



```

Qy 241 EVYSNPCLSEKPGIVYASLNHSLVGLNSRLARNVKEAPTEYASICVRS 289
|||
Db 241 EVYSNPCLSEKPGIVYASLNHSLVGLNSRLARNVKEAPTEYASICVRS 289

RESULT 2
US-10-987-663-10
; Sequence 10, Application US/10987663
; Publication No. US20050272118A1
; GENERAL INFORMATION:
; APPLICANT: GENENTECH, INC.
; APPLICANT: CLARK, HILARY
; APPLICANT: EATON, DANIEL L.
; APPLICANT: WRANIK, BERND
; APPLICANT: OUYANG, WENJUN
; APPLICANT: GONZALES, LINO
; APPLICANT: LOYET, KELLY M.
; TITLE OF INVENTION: Novel Compositions and Methods for the Treatment of
; TITLE OF INVENTION: Immune Related Diseases
; FILE REFERENCE: P1996R1P1-US
; CURRENT APPLICATION NUMBER: US/10/987,663
; CURRENT FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US 60/421,236
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 10/371,341
; PRIOR FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 10
; LENGTH: 295
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-987-663-10

Query Match 99.2%; Score 1539; DB 6; Length 295;
Best Local Similarity 98.0%; Pred. No. 5.7e-143;
Matches 289; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

Qy 1 MKTLPAMLGTGKLFVWFLLPYLDIWNHGHKESCDVLYIKRQSEHSILAGDPPELECPV 60
|||
Db 1 MKTLPAMLGTGKLFVWFLLPYLDIWNHGHKESCDVLYIKRQSEHSILAGDPPELECPV 60

Qy 61 KYCANRPHVTWCKLNGTTCTVKLEDROTQTSWKEEKNISPFILHFEFVLPNDNGSYRCSANFQ 120
|||
Db 61 KYCANRPHVTWCKLNGTTCTVKLEDROTQTSWKEEKNISPFILHFEFVLPNDNGSYRCSANFQ 120

Qy 121 SNLIESHSTTLVYT-----DVKSASRSPSKDEASRPWLLYSLLPLGGLPLLITTCFCL 174
|||
Db 121 SNLIESHSTTLVYTAFTNIPDVKSASRSPSKDEASRPWLLYSLLPLGGLPLLITTCFCL 180

Qy 175 FCCLRRHQGHQNELSDTAGREINLVDAHLKSEQTEASTRONSQVLLSTGTGYDNDPDLCP 234
|||
Db 181 FCCLRRHQGHQNELSDTAGREINLVDAHLKSEQTEASTRONSQVLLSTGTGYDNDPDLCP 240

Qy 235 RMQEGSEVYSNPCLEENKPGIVYASLNHSLVGLNSRLARNVKEAPTEYASICVRS 289
|||
Db 241 RMQEGSEVYSNPCLEENKPGIVYASLNHSLVGLNSRLARNVKEAPTEYASICVRS 295

RESULT 3
US-10-987-663-8
; Sequence 8, Application US/10987663
; Publication No. US20050272118A1
; GENERAL INFORMATION:
; APPLICANT: GENENTECH, INC.
; APPLICANT: CLARK, HILARY
; APPLICANT: EATON, DANIEL L.
; APPLICANT: WRANIK, BERND
; APPLICANT: OUYANG, WENJUN
; APPLICANT: GONZALES, LINO
; APPLICANT: LOYET, KELLY M.
; TITLE OF INVENTION: Novel Compositions and Methods for the Treatment of
; TITLE OF INVENTION: Immune Related Diseases
; FILE REFERENCE: P1996R1P1-US

```



GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 8, 2006, 16:48:30 ; Search time 26.5 Seconds  
(without alignments)  
1049.307 Million cell updates/sec

Title: US-10-600-997-6

Perfect score: 1552

Sequence: 1 MKTLPAMLTGKLFMWFFLI.....RLARNVKEAPTEYASICVRS 289

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 80:\*

2: pirl:\*

3: pirl3:\*

4: pirl4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	121	7.8	6642	2 T29757	protein UNC-89 - C
2	113.5	7.3	841	2 JCS894	killer cell inhibi
3	113	7.3	773	1 QRRRG	secretory componen
4	112	7.2	335	2 A53434	cell surface glyco
5	107.5	6.9	1036	2 S22383	axonin 1 precursor
6	102	6.6	1852	2 A37860	calcium channel pr
7	101.5	6.5	812	1 A36477	fibroblast growth
8	100.5	6.5	5175	2 T20992	hypothetical prote
9	100.5	6.5	5198	2 T43290	hemocentin precurs
10	99.5	6.4	1336	2 I60598	Fit-1 tyrosine kin
11	98	6.3	7962	2 I38346	elastic titin - hu
12	97.5	6.3	806	2 A35963	protein-tyrosine k
13	97.5	6.3	1158	2 S33901	reverse transcript
14	96	6.2	3707	2 S18252	heparan sulfate pr
15	95.5	6.2	814	1 A39752	fibroblast growth
16	95	6.1	978	1 A49814	protein-tyrosine k
17	95	6.1	1277	2 T30532	neural cell adhesi
18	93.5	6.0	210	2 S25657	T-cell surface gly
19	93.5	6.0	296	2 B53434	cell surface glyco
20	92.5	6.0	303	2 A40807	membrane glycoprot
21	92.5	6.0	480	2 A56182	fibroblast growth
22	92.5	6.0	1177	2 T16594	hypothetical prote
23	92.5	6.0	1507	2 T42631	breast cancer tumo
24	91.5	5.9	210	2 E46482	T-cell surface gly
25	91.5	5.9	221	2 C46482	T cell surface gly
26	91.5	5.9	246	2 T01073	T cell surface gly
27	91.5	5.9	570	2 A57535	intrileukin 1 recep
28	91.5	5.9	6805	2 S20901	titin - rabbit (fir
29	91	5.9	632	2 T18692	hypothetical prote

30 91 5.9 769 2 S36657 SWI6 protein - yea  
31 90.5 5.8 192 2 I39464 CD8 antigen - huma  
32 90.5 5.8 729 2 A56795 fibroblast growth  
33 90.5 5.8 733 2 I49293 fibroblast growth  
34 90.5 5.8 822 1 TVMSFG fibroblast growth  
35 90.5 5.8 822 2 I42889 fibroblast growth  
36 90.5 5.8 832 2 JH0393 fibroblast growth  
37 90 5.8 761 2 B69797 transcription regu  
38 90 5.8 1209 2 T42718 probable neural ce  
39 89.5 5.8 750 2 S41051 fibroblast growth  
40 89.5 5.8 1694 2 S50065 sialoadhesin - mou  
41 89.5 5.8 4391 2 A38096 perlecan precursor  
42 89 5.7 244 2 AD1834 isopenicenyli transf  
43 88.5 5.7 246 2 D46482 T-cell surface gly  
44 88.5 5.7 797 2 S38579 fibroblast growth  
45 88.5 5.7 813 1 A49123 fibroblast growth

## ALIGNMENTS

### RESULT 1

T29757

protein UNC-89 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 03-Dec-1999

C:Accession: T29757

R:Du, Z.; Le, T.T.; Wilson, R.

submitted to the EMBL Data Library, May 1997

A:Description: The sequence of C. elegans cosmid C09D1.

A:Reference number: Z20679

A:Accession: T29757

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-6642 <DUZ>

A:Cross-references: UNIPARC:UPI000017CF3C; EMBL:AF003131; PIDN:AAB54132.1; GSPDB:GN0001

A:Experimental source: strain Bristol N2; clone C09D1

C:Genetics:

A:Gene: CBSP:unc-89

A:Map position: 1

A:Introns: 17/2; 108/3; 154/2; 211/2; 265/3; 326/2; 352/3; 426/2; 454/1; 500/1; 537/1; /3; 5917/1; 6027/1; 6061/3; 6153/2; 6515/1; 6552/3; 6609/1

Query Match 7.8%; Score 121; DB 2; Length 6642;

Best Local Similarity 23.4%; Pred. No. 0.35;

Matches 48; Conservative 24; Mismatches 69; Indels 64; Gaps 7;

QY 27 NIHGK-----ESCDVQL-----YIKROSEHSILAGDPPELSCPVKYCAN 65  
Db 5574 NAHGKAKTQATAHVQWALGKTEKPKMDEGKPKFILELSDMSVSLGNVIDLECKVTGLPN 5633

QY 66 RPHVTWCKLNGTTCVKLEDRQTSWKEKNISFPILHPPEVLPNDGNSYVCSANFQSNLIE 125  
Db 5634 -PSVKMSKDGGL-----IEDSRFEWNSKSGVYQLRKIVATVHDEGTFCVATNENGSAT 5689

QY 126 SHS-----TLYTVDVKSASERPSKDE-----MASRPW----- 153  
Db 5690 TKSFVRMDGLSGGVVTASQPPRFTLKMGDVATTEGQPLKCKVDASLPENWVYKOGA 5749

QY 154 -----LLYSLLPLGGLPLITTC 171  
Db 5750 IVTPSDRIQISLSPDGVATLLIPSC 5774

### RESULT 2

JCS894

killer cell inhibitory receptor p91A precursor - mouse

C:Species: Mus musculus (house mouse)

C>Date: 18-Mar-1998 #sequence\_revision 18-Mar-1998 #text\_change 09-Jul-2004

C:Accession: JCS894

R:Yamashita, Y.; Fukuta, D.; Tsuji, A.; Nagabukuro, A.; Matsuda, Y.; Nishikawa, Y.; Ohy

J. Biochem. 123, 359-368, 1998

A>Title: Genomic structures and chromosomal location of p91, a novel murine regulatory

A:Reference number: JC5894; MUID:98218758; PMID:9538215  
A:Accession: JC5894  
A>Status: nucleic acid sequence not shown  
A:Molecule type: DNA  
A:Residues: 1-841 <YAM>  
A:Cross-references: UNIPROT:Q8R221; UNIPARC:UPI00000281E0; GB:AF040946  
C:Comment: This protein function as inhibitory cell-surface molecule against cell activation  
C:Genetics:  
A:Map position: 7  
F:1-23/Domain: signal sequence #status predicted <SIG>  
F:24-841/Product: killer cell inhibitory receptor p91A #status predicted <MAT>  
F:24-118,119-220,315-418,419-517,518-618/Domain: extracellular Ig-like #status predicted <TMM>  
F:636-674/Domain: transmembrane #status predicted <TMM>  
F:675-765/Domain: cytoplasmic #status predicted <CYT>  
Query Match 7.3%; Score 113.5; DB 2; Length 841;  
Best Local Similarity 20.1%; Pred. No. 0.12;  
Matches 67; Conservative 54; Mismatches 102; Indels 111; Gaps 15;  
QY 23 LDIWNHKGESCDVQIYIKRQSHSILAGDPFLECPVKYCANRPHVTWCKLNGTTCTV-- 80  
DB 512 LDIIL-ITGQLPLTPSLVK--PNHTVHSGTSTLLC-----WSMDSVDFTFILS 556  
QY 81 -----KLEDROTSMKEKNISFFILHPEPVLPNNGSYRC--SANFQSNLIE 125  
DB 557 KEGSAQOPLRLKSKSHDQGS--QAEFMSGAVTSHL-----SGYRCYGAONSSFYLLS 607  
QY 126 SHSTTLVYT---DVKSASRPSKDEMASRPMLYSLPLGLPLLL-----ITTCFCLFC 176  
DB 608 SASAPVELTVSGPIETSTPEPTMS-----MPLGLHMYLKALIGSVAFILFL 655  
QY 177 CL-----RRHQ-----KONELSDTAGREINLVDAHLKSEQTEASTRONSVLLSE 222  
DB 656 FILIFILLRRHRGKPRKDVQKQKOLQSGAEPT-----TRKGELOKRPNPAATQ 709  
QY 223 TGYDNDPDLCFRMQSGSEVSNPCLEENKPGIVYASLHNSVT----- 265  
DB 710 ESLIASVEDM--QTEGVLENSWTPPEEDPQGETYIAQVPSRLRKAGHVSPMSREQNLN 767  
QY 266 -----GLNSRLARNVKAPTEYASICVRS 289  
DB 768 TEYQAEQGGANNAQESGESQDVTYAQLCSRT 801

RESULT 3  
QRRBG  
secretory component precursor - rabbit  
N:Alternate names: poly-Ig receptor; polymeric immunoglobulin receptor  
N:Contains: free secretory component; transmembrane secretory component  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 15-Nov-1984 #sequence\_revision 15-Nov-1984 #text\_change 09-Jul-2004  
C:Accession: A02111; A28077  
R:Mostov, K.E.; Friedlander, M.; Blobel, G.  
Nature 308, 37-43, 1984  
A:Title: The receptor for transepithelial transport of IgA and IgM contains multiple immunoglobulin domains  
A:Reference number: A02111; MUID:84142246; PMID:6322002  
A:Accession: A02111  
A:Molecule type: mRNA  
A:Residues: 1-773 <NOS>  
A:Cross-references: UNIPROT:P01832; UNIPARC:UPI0000043E81; GB:K01291; NID:915  
A>Note: the authors translated the codon ACC for residue 54 as Asn  
R:Frutiger, S.; Hughes, G.J.; Hanly, W.C.; Jaton, J.C.  
J. Biol. Chem. 263, 8120-8125, 1988  
A:Title: Rabbit secretory components of different allotypes vary in their carbohydrate composition  
A:Reference number: A28077; MUID:88228032; PMID:3131339  
A:Accession: A28077  
A:Molecule type: protein  
A:Residues: 87-114; 410-424 <FRU>  
A:Cross-references: UNIPARC:UPI000017374B; UNIPARC:UPI000017374C  
C:Comment: This receptor binds polymeric IgA and IgM at the basolateral surface of epithelial cells. Cleavage occurs to separate the extracellular portion, also known as the secretory component, from the transmembrane portion. The five domains of the secretory component exhibit homology with immunoglobulin V regions. The similarity between the secretory component and immunoglobulin V regions leads to high or low molecular weight polymers.  
C:Comment: Alternative splicing in the extracellular domain leads to high or low molecular weight polymers.

C:Superfamily: secretory component; immunoglobulin homology  
C:Keywords: alternative splicing; duplication; glycoprotein; immunoglobulin receptor; P:  
F:1-18/Domain: signal sequence #status predicted <SIG>  
F:19-773/Product: transmembrane secretory component #status predicted <MAT>  
F:19-575/Domain: free secretory component #status predicted <MAT>  
F:30-647/Domain: extracellular #status predicted <EXT>  
F:39-117/Domain: immunoglobulin homology <IM1>  
F:148-227/Domain: immunoglobulin homology <IM2>  
F:253-326/Domain: immunoglobulin homology <IM3>  
F:362-440/Domain: immunoglobulin homology <IM4>  
F:471-540/Domain: immunoglobulin homology <IM5>  
F:648-670/Domain: transmembrane #status predicted <TMM>  
F:671-773/Domain: intracellular #status predicted <INT>  
F:46-115,155-225,260-324,369-438,478-538/Disulfide bonds: #status predicted  
F:108/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental  
F:418/Binding site: carbohydrate (Asn) (covalent) #status experimental  
Query Match 7.3%; Score 113; DB 1; Length 773;  
Best Local Similarity 20.8%; Pred. No. 0.12;  
Matches 52; Conservative 40; Mismatches 102; Indels 56; Gaps 11;  
QY 45 EHSIILAGDPFLEEC--PVKYCANRPHVTWCKLNGT-TCVCKLEDROTSMKE-----EKNISF 97  
DB 33 EWNVLGDSVSTCYPTTSVTRHSRKFPCREESGRCVTLASTGVTGQYSGRGLTDF 92  
QY 98 -----FILHPEPVLPNNGSYRCANFOSNLIESHTLYVTDVKSASRPSKDEMASRP 152  
DB 93 PDKGFVYTVDTQLTQNDSSGKYGNGRGLDFGVNVL-----VSQKPEPDDVYKQ 145  
QY 153 WLLYSLPLGLPLLTTCFCLFCLRRHQKONELSDTAGREINLVDAHLKSE----- 206  
DB 146 VESYTV-----TITCFYVATR-QLKSKFYKVEDGELVLIIDSSKSKADPRYK 193  
QY 207 -----QTEASTRONSVLLSETGIYDNDPDLCFRMQSGSEVSNPCLEENK-----PG 254  
DB 194 GRITLIQISTAKBFTVTIKHLQNDAGQYVC---QSGSD---PTAEQNVDLRLTPG 246  
QY 255 IYASLNHSV 264  
DB 247 LLYGNLGGSV 256  
RESULT 4  
A53434  
cell surface glycoprotein gp49B form 1 precursor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 19-May-1995 #sequence\_revision 19-May-1995 #text\_change 09-Jul-2004  
C:Accession: A53434  
R:Castells, M.C.; Wu, X.; Arn, J.P.; Austen, K.P.; Katz, H.R.  
J. Biol. Chem. 269, 8393-8401, 1994  
A:Title: Cloning of the gp49B gene of the immunoglobulin superfamily and demonstration of its relationship to the Ig gene  
A:Reference number: A53434; MUID:94179223; PMID:8132564  
A:Accession: A53434  
A>Status: preliminary  
A:Molecule type: DNA; mRNA  
A:Residues: 1-335 <CAS>  
A:Cross-references: UNIPROT:Q64281; UNIPARC:UPI000000189E; GB:U05265; NID:9475446; PION  
C:Genetics:  
A:Gene: gp49B  
A:Introns: 12/3; 24/2; 119/2; 220/1; 232/1; 271/1; 288/3; 311/1  
C:Keywords: alternative splicing; glycoprotein  
Query Match 7.2%; Score 112; DB 2; Length 335;  
Best Local Similarity 22.6%; Pred. No. 0.05;  
Matches 49; Conservative 37; Mismatches 65; Indels 66; Gaps 10;  
QY 88 SW-----KSEKNISPFILHPEPVLPNNGSYRCANFQSN-----LIESHTLYVTDV 136  
DB 164 SNTLDSQHQANQPSYATFVL--DAVTENHNGTFRCYGYFRNEPQWSPKSNLDMIS 221  
QY 137 KSASRPSKDEMASRPMLYSLPLGLPLLTTCFCLFCLRRHQ-GKQNELSDTAGRE 195  
DB 222 KQDSSTPTEDGLETQKILIGVL----VSFLLPLFLILIGYQYGHKK----- 269

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: February 8, 2006, 16:43:35 ; Search time 164 Seconds  
(without alignments)  
1243.279 Million cell updates/sec

Title: US-10-600-997-6  
Perfect score: 1552  
Sequence: 1 MKTLPAMLGKLFVFFLI.....RLARNVKEAPTEYASICVRS 289

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot\_05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1552	100.0	289	1	BTLA HUMAN
2	733.5	47.3	306	1	BTLA MOUSE
3	694.5	44.7	308	1	BTLA RAT
4	121	7.8	592	2	OSW615 CAEEL
5	121	7.8	632	1	UNC939 CAEEL
6	121	7.8	712	2	OSW616 CAEEL
7	121	7.8	744	2	OSW617 CAEEL
8	121	7.8	808	2	Q72120 CAEEL
9	119.5	7.7	266	2	Q9CUC8 MOUSE
10	119.5	7.7	343	1	SLAF1 MOUSE
11	119.5	7.7	343	2	Q544K1 MOUSE
12	118	7.6	1914	1	MYLK HUMAN
13	117	7.5	1914	2	Q5MY99 HUMAN
14	117	7.5	1914	2	Q724J0 HUMAN
15	115	7.4	841	2	P97484 MOUSE
16	113.5	7.3	841	2	Q8R221 MOUSE
17	113	7.3	773	1	PICR RABIT
18	112	7.2	335	1	LIRB4 MOUSE
19	107.5	6.9	1036	1	CNTN2 CHICK
20	107	6.9	1272	2	Q5G1T3 BRARE
21	105.5	6.8	265	2	Q81P93 DROME
22	105.5	6.8	298	2	Q96114 DROME
23	105	6.8	428	2	Q6F3J3 MOUSE
24	105	6.8	1272	2	Q4JDD5 BRARE
25	104.5	6.7	1845	2	Q5MYA0 HUMAN
26	103.5	6.7	1029	2	Q6ZJE3 ORYSA
27	103.5	6.7	1271	2	Q6U714 BRARE
28	103	6.6	376	2	Q67EV3 RAT
29	103	6.6	841	2	Q54999 MOUSE
30	103	6.6	1026	1	CNTN4 RAT
31	102	6.6	532	2	Q4Q815 LEISHMA

32	102	6.6	1852	1	CACIS CYPCA
33	101.5	6.5	810	2	Q9PS96 XENLA
34	101.5	6.5	812	1	EGFR1 XENLA
35	100.5	6.5	335	2	Q90746 CHICK
36	100.5	6.5	838	1	SEM4G HUMAN
37	100.5	6.5	838	2	Q58BY1 HUMAN
38	100.5	6.5	5175	2	Q810L3 CAEEL
39	100.5	6.5	5198	2	Q76518 CAEEL
40	99.5	6.4	326	2	Q8CAU4 MOUSE
41	99.5	6.4	904	2	Q4HXS1 GIBZE
42	99.5	6.4	1336	1	VGFR1 RAT
43	99	6.4	3950	2	Q7YRF5 CANFA
44	99	6.4	10495	2	Q4RE92 TETNG
45	98	6.3	837	1	SEM4G MOUSE

P22316	cyprinus ca
Q9PS96	xenopus lae
P22182	xenopus lae
Q90746	gallus gall
Q9NTN9	homo sapien
Q58EY1	homo sapien
Q810L3	caenorhabdi
Q76518	caenorhabdi
Q8CAU4	mus muscucu
Q4HXS1	gibberella
P53767	rattus norv
Q7YRF5	canis famil
Q4RE92	tetraodon n
Q9WUH7	mus muscucu

## ALIGNMENTS

RESULT 1					
BTLA HUMAN					
ID	BTLA HUMAN	STANDARD;	PRT;	289 AA.	
AC	Q7Z6A9; Q6ZNH9;				
DT	13-SEP-2005 (Rel. 48, Created)				
DT	13-SEP-2005 (Rel. 48, Last sequence update)				
DT	13-SEP-2005 (Rel. 48, Last annotation update)				
DE	B and T lymphocyte attenuator precursor (B and T lymphocyte-associated protein).				
DE	Name=BTLA;				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;				
OC	Homo				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	TYR-282, N-GLYCOSYLATION, FUNCTION, AND INTERACTIONS WITH PTPN6 AND PTPN11.				
RX	PubMed=12796776; DOI=10.1038/nr1944;				
RA	Watanabe N., Gavrieli M., Sedy J.R., Yang J., Fallarino F.,				
RA	Loftin S.K., Hurchla M.A., Zimmerman N., Sim J., Zang X., Murphy T.L.,				
RA	Russell J.H., Allison J.P., Murphy K.M.;				
RT	"BTLA is a lymphocyte inhibitory receptor with similarities to CTLA-4 and PD-1."				
RL	Nat. Immunol. 4:670-679(2003).				
RN	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 4-289.				
RX	TISSUE=Trachea;				
RX	PubMed=14702039; DOI=10.1038/ng1285;				
RA	Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,				
RA	Wakanatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,				
RA	Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,				
RA	Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,				
RA	Nagahara K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,				
RA	Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,				
RA	Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,				
RA	Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,				
RA	Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,				
RA	Fujimori K., Tanai H., Kimata M., Watanabe M., Hirao K., Chiba Y.,				
RA	Ishida S., Ono Y., Takiguchi S., Watanabe S., Yoshida M., Hota T.,				
RA	Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,				
RA	Nomura Y., Togliya S., Komai F., Hara R., Takeuchi K., Arita M.,				
RA	Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,				
RA	Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,				
RA	Moriya S., Momiya H., Satoh N., Takami S., Terashima Y., Suzuki O.,				
RA	Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,				
RA	Hishigaki H., Watanabe T., Sugiyama A., Takenoto M., Kawakami B.,				
RA	Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,				
RA	Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,				
RA	Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,				
RA	Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,				
RA	Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,				
RA	Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,				

RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,  
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,  
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,  
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isegai T., Sugano S.,  
RT "Complete sequencing and characterization of 21,243 full-length human  
RT cDNAs";  
RL Nat. Genet. 36:40-45(2004).  
RN [3]  
RN MUTAGENESIS OF TYR-226; TYR-257 AND TYR-282, AND INTERACTIONS WITH  
RP PTPN6 AND PTPN11.  
RX PubMed=14652006; DOI=10.1016/j.bbrc.2003.11.070;  
RA Gavioli M., Watanabe N., Loftin S.K., Murphy T.L., Murphy K.M.,  
RT "Characterization of phosphotyrosine binding motifs in the cytoplasmic  
RT domain of B and T lymphocyte attenuator required for association with  
RT protein tyrosine phosphatases SHP-1 and SHP-2";  
RL Biochem. Biophys. Res. Commun. 312:1236-1243(2003).  
RN [4]  
RN INTERACTION WITH TNFRSF14, AND PHOSPHORYLATION.  
RX PubMed=15568026; DOI=10.1038/nrl144;  
RA Sedy J.R., Gavioli M., Potter K.G., Hurchla M.A., Lindsley R.C.,  
RA Hildner K., Scheu S., Pfeiffer K., Ware C.F., Murphy T.L., Murphy K.M.,  
RT "B and T lymphocyte attenuator regulates T cell activation through  
RT interaction with herpesvirus entry mediator";  
RL Nat. Immunol. 6:90-98(2005).  
CC -1- FUNCTION: Lymphocyte inhibitory receptor which inhibits  
CC lymphocytes during immune response.  
CC -1- SUBUNIT: Interacts with tyrosine phosphatases PTPN6/SHP-1 and  
CC PTPN11/SHP-2. Interacts with TNFRSF14/HVEM.  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).  
CC -1- PTM: Phosphorylated on Tyr residues by TNFRSF14 and by antigen  
CC receptors crosslinking, both inducing association with PTPN6 and  
CC PTPN11.  
CC -1- PTM: N-glycosylated.  
CC -1- SIMILARITY: Contains 1 Ig-like V-type (immunoglobulin-like)  
CC domain.  
CC -----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
DR EMBL; AV293286; AAP44003.1; -; mRNA.  
DR EMBL; AK131204; BAD18396.1; ALT\_INIT; mRNA.  
DR Ensembl; ENSG00000186265; Homo sapiens.  
DR HGNC; HGNC:21087; BTLA.  
DR MIM; 607925; -.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00409; Ig; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
KW Glycoprotein; Immune response; Immunoglobulin domain; Phosphorylation;  
KW Receptor; Signal; Transmembrane.  
FT SIGNAL 1 30 Potential.  
FT CHAIN 31 289 B and T lymphocyte attenuator.  
FT TOPO\_DOM 31 157 Extracellular (Potential).  
FT TRANSMEM 158 178 Potential.  
FT TOPO\_DOM 179 289 Cytoplasmic (Potential).  
FT DOMAIN 43 134 Ig-like V-type.  
FT CARBOHYD 75 75 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 94 94 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 110 110 N-linked (GlcNAc...) (Potential).  
FT DISULFID 34 63 By similarity.  
FT DISULFID 58 115 By similarity.  
FT MUTAGEN 226 226 Y->F: No change of phosphorylation  
FT implicated in interaction with PTPN6 and  
FT PTPN11. Severe reduction of  
FT phosphorylation; when associated with P-  
FT 257 and/or F-282.  
FT Y->F: No change of phosphorylation  
FT implicated in interaction with PTPN6 and  
FT PTPN11. Severe reduction of

FT phosphorylation; when associated with P-  
FT 226 and/or F-282.  
FT Y->F: No change of phosphorylation  
FT implicated in interaction with PTPN6 and  
FT PTPN11. Severe reduction of  
FT phosphorylation; when associated with P-  
FT 226 and/or F-257.  
FT V -> M (in Ref. 1).  
FT CONFLICT 105 105  
FT CONFLICT 138 138  
FT CONFLICT 148 148 M -> G (in Ref. 1).  
FT CONFLICT 171 171 M -> W (in Ref. 1).  
FT CONFLICT 219 219 L -> P (in Ref. 2).  
FT CONFLICT 223 223 T -> A (in Ref. 1).  
FT CONFLICT 243 243 Y -> C (in Ref. 1).  
SQ SEQUENCE 289 AA; 32781 MW; 98D1FE325D882642 CRC64;  
Query Match 100.0%; Score 1552; DB 1; Length 289;  
Best Local Similarity 100.0%; Pred. No. 1.9e-123;  
Matches 289; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKTLPAMLTGKLFVWFLLPYLDIWNTHGKSCDQVLYIKRQSEHSILAGDPFELCPV 60  
DB 1 MKTLPAMLTGKLFVWFLLPYLDIWNTHGKSCDQVLYIKRQSEHSILAGDPFELCPV 60  
QY 61 KYCANRPHVTWCKLNGTTCVKLEDRQTSWKEKNISFFILHPEPVPNDNGSYRCSANFQ 120  
DB 61 KYCANRPHVTWCKLNGTTCVKLEDRQTSWKEKNISFFILHPEPVPNDNGSYRCSANFQ 120  
QY 121 SNLISHSTTLVTDVKASERPSKDEASRPWLYSLPLGGLPLLITTCFLCCLLR 180  
DB 121 SNLISHSTTLVTDVKASERPSKDEASRPWLYSLPLGGLPLLITTCFLCCLLR 180  
QY 181 HGKQNELSDTAGREINLVDAHLKSEQTEASTRQNSQVLLSTGTIYDNDPDLCFRMEQS 240  
DB 181 HGKQNELSDTAGREINLVDAHLKSEQTEASTRQNSQVLLSTGTIYDNDPDLCFRMEQS 240  
QY 241 EYVSNPCLEENKPGIYVYSLNHSVIGINSRLRNKVEAPTEYASICVRS 289  
DB 241 EYVSNPCLEENKPGIYVYSLNHSVIGINSRLRNKVEAPTEYASICVRS 289  
RESULT 2  
BTLA\_MOUSE  
ID BTLA\_MOUSE STANDARD; PRT; 306 AA.  
AC Q7TSA3;  
DT 13-SEP-2005 (Rel. 48, Created)  
DT 13-SEP-2005 (Rel. 48, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE B and T lymphocyte attenuator precursor (B and T lymphocyte-associated  
DE protein).  
GN Name=Btla;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2), MUTAGENESIS OF TYR-245;  
RP TYR-274 AND TYR-299, N-GLYCOSYLATION, TISSUE SPECIFICITY, INTERACTIONS  
RP WITH PTPN6 AND PTPN11, AND VARIANTS GLU-41; 45-ASN--LYS-47; HIS-52;  
RP TRP-55; GLU-63; TRP-85; GLY-91 AND ARG-102.  
RC STRAIN=129/SVSV;  
RX PubMed=1296776; DOI=10.1038/nj944;  
RA Watanabe N., Gavioli M., Sedy J.R., Yang J., Fallarino F.,  
RA Loftin S.K., Hurchla M.A., Zimmerman N., Sim J., Zang X., Murphy T.L.,  
RA Russell J.H., Allison J.P., Murphy K.M.,  
RT "BTLA is a lymphocyte inhibitory receptor with similarities to CTLA-4  
RT and PD-1";  
RL Nat. Immunol. 4:670-679(2003).  
RN [2]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 3), AND VARIANT  
RP THR-143  
RP STRAIN=CS7BL/6J; TISSUE=Thymus;

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 10, 2006, 05:19:46 ; Search time 649 Seconds  
(without alignments)  
8934.180 Million cell updates/sec

Title: US-10-600-997-7  
Perfect score: 870  
Sequence: 1 atgaagacattgcctgcat.....ccatattgtgaggagtaa 870

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues  
Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_21.\*  
1: Geneseqn1980s.\*  
2: Geneseqn1990s.\*  
3: Geneseqn2000s.\*  
4: Geneseqn2001as.\*  
5: Geneseqn2001bs.\*  
6: Geneseqn2002as.\*  
7: Geneseqn2002bs.\*  
8: Geneseqn2003as.\*  
9: Geneseqn2003bs.\*  
10: Geneseqn2003cs.\*  
11: Geneseqn2003ds.\*  
12: Geneseqn2004as.\*  
13: Geneseqn2004bs.\*  
14: Geneseqn2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	870	100.0	870	12	ADH34663	Adh34663 Human BTL
2	870	100.0	870	14	ADX01460	Adx01460 Human tol
3	857.2	98.5	870	13	ADU51091	Adu51091 Human spl
4	857.2	98.5	990	13	ADU51153	Adu51153 Human spl
5	854	98.2	916	12	ADH74501	Adh74501 Human mcd
6	854	98.2	1066	12	ADO43715	Ado43715 Nucleotid
7	854	98.2	1066	14	AEA23329	Aea23329 Tumor ant
8	846	97.2	3002	12	ADH74499	Adh74499 Human mcd
9	833	95.7	849	12	ADH74497	Adh74497 Human mcd
10	764.2	87.8	777	13	ADU51090	Adu51090 Human spl
11	704.2	80.9	717	13	ADU51089	Adu51089 Human SPE
12	564	64.8	1014	6	AB876365	Ab876365 DNA encod
13	527.6	60.6	534	13	ADU51085	Adu51085 Human SPE
14	520.2	59.8	726	2	AAV88865	Aav88865 EST clone
15	466.2	53.6	471	13	ADU51083	Adu51083 Human SPE
16	437.6	50.3	444	13	ADU51084	Adu51084 Human SPE
17	425	48.9	769	14	ADY19217	Ady19217 DNA encod
18	402.8	46.3	1903	2	AZ00830	Az00830 Human sec
19	402.8	46.3	1903	8	ADA40232	Ada40232 Human sec

20	402.8	46.3	1903	10	ADA56392	Ada56392 Gene enco
21	388	44.6	396	13	ADU51088	Adu51088 Human SPE
22	378	43.4	1940	2	AZ00850	Az00850 Human sec
23	378	43.4	1940	8	ADA40551	Ada40551 Human sec
24	378	43.4	1940	10	ADA56697	Ada56697 Gene enco
25	376.2	43.2	381	13	ADU51082	Adu51082 Human SPE
26	326.6	37.5	333	13	ADU51087	Adu51087 Human spl
27	276.6	31.8	422	10	ADP81166	Adp81166 Leukaemia
28	276.6	31.8	465	10	ADP82536	Adp82536 Leukaemia
29	275.6	31.7	921	12	ADH34665	Adh34665 Mouse BTL
30	270.6	31.1	3229	14	ADX01473	Adx01473 Human tol
31	267.6	30.8	921	13	ADU51133	Adu51133 Murine sp
32	267.6	30.8	1250	13	ADU51154	Adu51154 Murine sp
33	267.6	30.8	1276	13	ADU51158	Adu51158 Murine sp
34	264.6	30.4	957	13	ADU51155	Adu51155 Murine sp
35	264.6	30.4	1722	13	ADU51156	Adu51156 Murine sp
36	254.2	29.2	831	13	ADU51132	Adu51132 Murine sp
37	236.8	27.2	750	13	ADU51131	Adu51131 Murine SP
38	233	26.8	319	3	AAC02957	Aac02957 Human sec
39	199.4	22.9	201	13	ADU51073	Adu51073 Human spl
40	198.4	22.8	201	13	ADU51086	Adu51086 Human SPE
41	157.2	18.1	537	13	ADU51138	Adu51138 Murine SP
42	157.2	18.1	537	13	ADU51162	Adu51162 Murine sp
43	156.4	18.0	378	13	ADU51130	Adu51130 Murine SP
44	149.2	17.1	540	13	ADU51125	Adu51125 Murine SP
45	149.2	17.1	612	13	ADU51127	Adu51127 Murine SP

ALIGNMENTS

RESULT 1  
ADH34663  
ID ADH34663 standard; cDNA; 870 BP.  
XX  
AC ADH34663;  
XX  
DT 11-MAR-2004 (first entry)  
XX  
DE Human BTLA coding sequence.  
XX  
KW B7x; ligand; B and T lymphocyte attenuator; BTLA; tumour; inhibition;  
KW tumour-specific; immunological tolerance; cancer; autoimmune disease;  
KW diabetes; pre-eclampsia; rheumatoid arthritis; multiple sclerosis;  
KW infection; graft rejection; cell cycle progression; differentiation;  
KW survival; cytokine production; cytolytic activation;  
KW antigen presentation; antibody production; ss; gene.  
XX  
OS Homo sapiens.  
XX  
FH Key  
FT CDS  
FT Location/Qualifiers  
FT 1..870  
FT /\*tag= a  
FT /product= "Human BTLA"  
FT  
FT WO2004000221-A2.  
XX  
PD 31-DEC-2003.  
XX  
XX  
XX 20-JUN-2003; 2003WO-US019614.  
XX  
XX 20-JUN-2002; 2002US-0390653P.  
XX  
XX 06-JAN-2003; 2003US-0438593P.  
XX  
XX (REGC ) UNIV CALIFORNIA.  
XX (UNIW ) UNIV WASHINGTON.  
XX  
XX Allison JP, Murphy KP, Watanabe N, Murphy TL, Yang J, Zang X;  
XX WPI; 2004-082409/08.  
XX P-PSDB; ADH34662.  
XX  
XX New recombinant B and T lymphocyte attenuator nucleic acid and protein,

PT useful for modulating B and T lymphocyte activity, or for diagnosing and  
 PT treating cancer, autoimmune disease or infectious disease.  
 XX Claim 64; Fig 28; 121pp; English.

XX This sequence encodes a human B and T lymphocyte attenuator (BTLA). BTLA  
 CC acts as a negative regulator of both B and T lymphocyte activity, where  
 CC signaling mediated by BTLA results in the inhibition of BTLA-positive  
 CC lymphocyte activity. In BTLA-positive T cells BTLA signalling can inhibit  
 CC TCR-induced T cell responses, such as cell cycle progression,  
 CC differentiation, survival, cytokine production and cytolytic activation.  
 CC In BTLA-positive B cells BTLA signalling can inhibit B cell antigen  
 CC receptor-induced B cell responses, such as cell cycle progression,  
 CC differentiation, survival, antigen presentation and antibody production.  
 CC B7x is a ligand for the recombinant BTLA of the invention. B7x is able to  
 CC negatively regulate B and T lymphocyte activity through its interaction  
 CC with BTLA, which inhibits both B and T cell responses. Therefore B7x  
 CC positive tumour tissue inhibits the activity of tumour-specific T cells.  
 CC B7x is also expressed on non-tumour non-lymphoid tissue, showing that the  
 CC B7x/BTLA interaction is a mechanism for maintaining immunological  
 CC tolerance. BTLA proteins and related nucleic acids are useful for  
 CC modulating B and T lymphocyte activity, for diagnosing and treating  
 CC cancer, autoimmune disease, e.g. diabetes, pre-eclampsia, rheumatoid  
 CC arthritis or multiple sclerosis, or infectious disease, or for preventing  
 CC acute and/or chronic graft rejection.

SQ Sequence 870 BP; 272 A; 185 C; 185 G; 228 T; 0 U; 0 Other;

Query Match		100.0%;	Score 870;	DB 12;	Length 870;	
Best Local Similarity		100.0%;	Pred. No. 5.5e-251;			
Matches 870;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1	ATGAGACATGCTCCCATCTGTTGGAACATGGGAATTAATTTGGTCTCTCTTAATC	60			
DB	1	ATGAGACATGCTCCCATCTGTTGGAACATGGGAATTAATTTGGTCTCTCTTAATC	60			
QY	61	CCATATCTGGACATCTGGAACATCCATGGGAAGATCATGTGATGACGCTTTATATA	120			
DB	61	CCATATCTGGACATCTGGAACATCCATGGGAAGATCATGTGATGACGCTTTATATA	120			
QY	121	AAGAGACAATCTGAAACATCTCCATCTTAGCAGGAGATCCCTTTGAACTAGAAATGCTGTG	180			
DB	121	AAGAGACAATCTGAAACATCTCCATCTTAGCAGGAGATCCCTTTGAACTAGAAATGCTGTG	180			
QY	181	AAATCTGTGCTAAAGGCTCATGTGACATGTTGTCAGCTCATGTCAGTGAATGTGTA	240			
DB	181	AAATCTGTGCTAAAGGCTCATGTGACATGTTGTCAGCTCATGTCAGTGAATGTGTA	240			
QY	241	AAACTTGAAGATAGACAAACAGTTGGAAGGAGAGAGAAACATTTTCATTTTCAATCTA	300			
DB	241	AAACTTGAAGATAGACAAACAGTTGGAAGGAGAGAGAAACATTTTCATTTTCAATCTA	300			
QY	301	CATTTTGAACCAATGCTTCTTAATGACATGCTCATACCGCTGTTCTGCAAAATTTTCAG	360			
DB	301	CATTTTGAACCAATGCTTCTTAATGACATGCTCATACCGCTGTTCTGCAAAATTTTCAG	360			
QY	361	TCTAATCTCATTTGAAGCCATCAACATCTTTATGTGACAGATGTAAGAGTGGCTCA	420			
DB	361	TCTAATCTCATTTGAAGCCATCAACATCTTTATGTGACAGATGTAAGAGTGGCTCA	420			
QY	421	GAACGACCTTCCAGGACCAAGTGGCAAGCAGACCTGGCTCTGTATAGTTTACTTCTCT	480			
DB	421	GAACGACCTTCCAGGACCAAGTGGCAAGCAGACCTGGCTCTGTATAGTTTACTTCTCT	480			
QY	481	TTGGGGGGATGCTCTTACTCATCTACCTGTTCTGCTGTTCTGCTGCTGCTGAGAAG	540			
DB	481	TTGGGGGGATGCTCTTACTCATCTACCTGTTCTGCTGTTCTGCTGCTGCTGAGAAG	540			
QY	541	CACCAAGGAAGCAAAATGAACTCTCTGACACAGCAGGAGGGAATTAATCTGGTTGAT	600			
DB	541	CACCAAGGAAGCAAAATGAACTCTCTGACACAGCAGGAGGGAATTAATCTGGTTGAT	600			
QY	601	GCTCACCTTTAAGAGCGCAACAGAGCAAGCAGCAGGCAAAATTTCCCAAGTACTGCTA	660			

DB	601	GCTCACCTTTAAGAGCGCAACAGAGCAAGCAGCAGGCAAAATTTCCCAAGTACTGCTA	660			
QY	661	TCAGAAAGCTGGAATTTATGATTAATGACCTGACCTTTGTTTTCAGGATGAGGAAGGCTT	720			
DB	661	TCAGAAAGCTGGAATTTATGATTAATGACCTGACCTTTGTTTTCAGGATGAGGAAGGCTT	720			
QY	721	GAAAGTTGTTCTTAATCCATGCTGGAAGAAACAAACAGGCAATTTGTTATGCTTCCCTG	780			
DB	721	GAAAGTTGTTCTTAATCCATGCTGGAAGAAACAAACAGGCAATTTGTTATGCTTCCCTG	780			
QY	781	AACCAATCTGTCATTTGGAATCAAGACTGGAAGAAATGTAAGAAAGCAACCAACA	840			
DB	781	AACCAATCTGTCATTTGGAATCAAGACTGGAAGAAATGTAAGAAAGCAACCAACA	840			
QY	841	GAATATGATCCATATGTTGAGGAGTTAA	870			
DB	841	GAATATGATCCATATGTTGAGGAGTTAA	870			

RESULT 2  
 ADX01460

ID ADX01460 standard; DNA; 870 BP.

XX AC ADX01460;

XX DT 21-APR-2005 (first entry)

XX DE Human tolerance target molecule #33.

XX Screening; immune disorder; autoimmune disease; transplant rejection;  
 KW diabetes mellitus; arthritis; rheumatoid arthritis; multiple sclerosis;  
 KW myasthenia gravis; systemic lupus erythematosus; Hashimoto's disease;  
 KW dermatitis; psoriasis; ulcerative colitis; scleroderma;  
 KW female genital tract inflammation; Crohn's disease; sarcoidosis;  
 KW pulmonary fibrosis; immunosuppressive; antidiabetic; antihypertensive;  
 KW antirheumatic; neuroprotective; muscular-gen.; antiinflammatory;  
 KW dermatological; antihypertensive; antipsoriatic; antiulcer;  
 KW gastrointestinal-gen.; respiratory-gen.; cytostatic; virucide; gene; ds.

XX OS Homo sapiens.

XX PN WO2005010215-A2.

XX PD 03-FEB-2005.

XX PF 19-JUL-2004; 2004WO-US023309.

XX PR 17-JUL-2003; 2003US-0488502P.

XX XX (TOLLE-) TOLERRX INC.

XX PI Rao P, Snyder J, Bagley A;

XX XX WPI; 2005-123168/13.

XX DR Identifying a tolerance modulatory compound, useful for reducing T  
 XX effector (Teff) cell function or increasing T regulatory (Treg) cell  
 XX function, by assaying for expression or activity of Treg marker and Teff  
 XX marker.

XX PS Disclosure; SEQ ID NO 33; 149pp; English.

XX CC The invention relates to a method of identifying a tolerance modulatory  
 CC compound comprising assaying for expression or activity of at least one T  
 CC regulatory (Treg) marker and at least one T effector (Teff) marker, where  
 CC a change in expression or activity of the Treg marker or the Teff marker  
 CC and/or an inverse change in expression or activity of the Teff marker  
 CC identifies the test compound as a tolerance modulatory compound. The  
 CC method comprises contacting a T cell with a stimulating agent and a test  
 CC compound and assaying for expression or activity of at least one Treg  
 CC marker and at least one Teff marker. The invention also relates to a  
 CC method of identifying a tolerance promoting compound and a method of

Db  
181 AAATACTGTGCTAACAGGCCTCATGTGACTTGGTGCAGCTCAATGGAAACAACATGTGTA 240





GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 10, 2006, 05:26:42 ; Search time 4815 Seconds  
(without alignments)  
10270.779 Million cell updates/sec

Title: US-10-600-997-7

Perfect score: 870

Sequence: 1 atgaagacattgcctgccat.....ccatattgtgtgaggagtgtaa 870

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5881141 seqs, 2842172553 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:\*

1: gb\_ba:\*

2: gb\_in:\*

3: gb\_env:\*

4: gb\_om:\*

5: gb\_ov:\*

6: gb\_pat:\*

7: gb\_ph:\*

8: gb\_pr:\*

9: gb\_ro:\*

10: gb\_sta:\*

11: gb\_sy:\*

12: gb\_un:\*

13: gb\_vi:\*

14: gb\_htg:\*

15: gb\_pl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	870	100.0	870	8	AY293286 Homo sapi
2	857.2	98.5	870	6	CQ947366 Sequence
3	857.2	98.5	990	6	CQ947428 Sequence
4	854	98.2	1066	6	CS105855 Sequence
5	846	97.2	3002	8	AK131204 Homo sapi
6	764.2	87.8	777	6	CQ947365 Sequence
7	704.2	80.9	717	6	CQ947364 Sequence
8	527.6	60.6	534	6	CQ947360 Sequence
9	520.2	59.8	726	6	BD060983 Secreted
10	466.2	53.6	471	6	CQ947358 Sequence
11	437.6	50.3	444	6	CQ947359 Sequence
12	425	48.9	769	6	CS035517 Sequence
13	425	48.9	769	6	CS044469 Sequence
14	402.8	46.3	1903	6	BD131124 45 human
15	402.8	46.3	1903	6	CS132603 Sequence
16	402.8	46.3	1903	6	AR339778 Sequence
17	388	44.6	396	6	CQ947363 Sequence
18	378	43.4	1940	6	BD131144 45 human

19	378	43.4	1940	6	CS132623	CS132623 Sequence
20	378	43.4	1940	6	AR339797	AR339797 Sequence
21	376.2	43.2	381	6	CQ947357	CQ947357 Sequence
22	326.6	37.5	333	6	CQ947362	CQ947362 Sequence
23	315.8	36.3	127852	8	AC092894	AC092894 Homo sapi
24	315.8	36.3	143094	14	AC024131	AC024131 Homo sapi
25	315.8	36.3	175135	14	AC079211	AC079211 Homo sapi
26	285.2	32.8	2230	9	BC092588	BC092588 Rattus no
27	276.6	31.8	422	6	AX779565	AX779565 Sequence
28	276.6	31.8	465	6	AX780935	AX780935 Sequence
29	275.6	31.7	921	9	AY293285	AY293285 Mus muscu
30	267.6	30.8	921	6	CQ947408	CQ947408 Sequence
31	267.6	30.8	1250	6	CQ947429	CQ947429 Sequence
32	267.6	30.8	1276	6	CQ947433	CQ947433 Sequence
33	264.6	30.4	957	6	CQ947430	CQ947430 Sequence
34	264.6	30.4	1722	6	CQ947431	CQ947431 Sequence
35	258.8	29.7	927	9	AY590499	AY590499 Rattus no
36	254.2	29.2	831	6	CQ947407	CQ947407 Sequence
37	236.8	27.2	750	6	CQ947406	CQ947406 Sequence
38	233	26.8	319	6	BD026702	BD026702 Sequence
39	233	26.8	319	6	AX887092	AX887092 Sequence
40	199.4	22.9	201	6	CQ947348	CQ947348 Sequence
41	198.4	22.8	201	6	CQ947361	CQ947361 Sequence
42	157.2	18.1	537	6	CQ947413	CQ947413 Sequence
43	157.2	18.1	537	6	CQ947437	CQ947437 Sequence
44	156.4	18.0	378	6	CQ947405	CQ947405 Sequence
45	149.2	17.1	540	6	CQ947400	CQ947400 Sequence

## ALIGNMENTS

RESULT 1	AY293286	Homo sapiens B and T lymphocyte attenuator (BTLA) mRNA, complete cds.	870 bp	linear	PRI 18-JUN-2003
LOCUS	AY293286				
DEFINITION	AY293286.1	GI:31880026			
ACCESSION	AY293286				
VERSION	AY293286.1				
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Homo sapiens				
REFERENCE					
AUTHORS	Watanabe,N., Gavriel,M., Sedy,J.R., Yang,J., Yang,J., Fallarino,F., Loftin,S.K., Hurchla,M.A., Zimmerman,N., Sim,J., Zang,X., Murphy,T.L., Russell,J.H., Allison,J.P. and Murphy,K.M.				
TITLE	BTLA is a lymphocyte inhibitory receptor with similarities to CTLA-4 and PD-1				
JOURNAL	Nat. Immunol.	(2003)	In press		
REFERENCE	2	(bases 1 to 870)			
AUTHORS	Murphy,K.M., Watanabe,N., Yang,J. and Murphy,T.L.				
TITLE	Direct Submission				
JOURNAL	Submitted (08-MAY-2003)	Pathology, Washington University, 660 S. Euclid, St. Louis, MO 63110, USA			
FEATURES					
source					
	1..870				
	/organism="Homo sapiens"				
	/mol_type="mRNA"				
	/db_xref="taxon:9606"				
	/cell_line="Ramos"				
	1..870				
	/gene="BTLA"				
	/note="immunoregulatory inhibitory receptor; similar to CTLA-4 and PD-1"				
gene					
CDS					
	1..870				
	/product="B and T lymphocyte attenuator"				
	/protein_id="AAP44003.1"				
	/db_xref="GI:31880027"				



Result No.	Query			ID	Description
	Score	Match	Length		
1	402.8	46.3	1903	3	US-09-369-247-39
2	402.8	46.3	1903	3	US-10-062-548-39
3	378	43.4	1940	3	US-09-369-247-58
4	378	43.4	1940	3	US-10-062-548-58
5	233	26.8	319	3	US-09-513-999C-2955
6	39.4	4.5	248968	3	US-09-949-016-12614
7	39.4	4.5	250958	3	US-09-949-016-16061
8	38	4.4	225127	3	US-09-949-016-16480
9	36.8	4.2	1137	3	US-09-543-681A-3307
10	36.6	4.2	832	3	US-09-621-976-2813
11	36.4	4.2	4305	3	US-09-645-593-1
12	36	4.1	832	3	US-09-621-976-2813
13	35.8	4.1	27425	3	US-09-524-101D-18
14	35.8	4.1	451924	3	US-09-949-016-12896
15	35.8	4.1	451925	3	US-09-949-016-17305
16	35.6	4.1	1664976	3	US-08-916-421B-1
17	35.6	4.1	1664976	3	US-09-693-570-1
18	35.4	4.1	2902	3	US-09-710-279-3489
19	35.4	4.1	235452	3	US-09-949-016-13675
20	34.8	4.0	88490	3	US-09-949-016-13758
21	34.8	4.0	88736	3	US-09-949-016-14222
22	34.4	4.0	399	3	US-09-621-976-8976
23	34.4	4.0	580073	3	US-08-545-528B-3
24	34.2	3.9	1191	3	US-09-107-532A-1085

Qy	241	AAACTTGAAGATAGACAAACCAAGTTGGAAGGAGAGAAACATTTTCATTTTCATTTCTA	300
Db	292	AAACTTGAAGATAGACAAACCAAGTTGGAAGGAGAGAGAAACATTTTCATTTTCATTTCTA	351
Qy	301	CATTTTGAACCAATGCTTCTTAATGACAAATGGGTCAATACCGTGTTCTGCAAAATTTTCAG	360
Db	352	CATTTTGAACCAAGTCTTCTTAATGACAAATGGGTCAATACCGTGTTCTGCAAAATTTTCAG	411
Qy	361	TCTAATCTCATTGAAAGCGCACTCAACAACTCTTTATGTGACAGATG	406
Db	412	TCTAATCTCATTGAAAGCGCACTCAACAACTCTTTATGTGACAGATG	457

```

RESULT 2
US-10-062-548-39
; Sequence 39 Application US/10062548
; Patent No. 6924356
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 44 Human Secreted Proteins
; FILE REFERENCE: P2024P1

```

Query Match	46.3%	Score 402.8;	DB 3;	Length 1903;
Best Local Similarity	99.5%;	Pred. NO. 2.8e-110;		
Matches 404;	Conservative	0;	Mismatches 2;	Indels 0;
				Gaps 0

Qy	61	CCATATCTGGACATCTGGAA	CATCCATGGAAAGAA	TCACTGATGTACAGCTTTATATA	120
Dp	112	CCATATCTGGACATCTGGAA	CATCCATGGAAAGAA	TCACTGATGTACAGCTTTATATA	171

Qy	121	172	231
Db	AAGAGACAACTCTGAA	CCTCCATCTTTAGCAGGAGATCCCTTTGAACTAGAGATGCCCTGTG	180
Db	AAGAGACAACTCTGAA	CCTCCATCTTTAGCAGGAGATCCCTTTGAACTAGAGATGCCCTGTG	231

	Qy	Db
181	AAATACTGTGCTAACAGGCTCATCTGACTTGGTCAAGCTCAATCGAACACATCTGTA	240
232	AAATACTGTGCTAACAGGCTCATCTGACTTGGTCAAGCTCAATCGAACACATCTGTA	291

Qy	Db
241	292
300	351

Db	352	351	366	411
QY	CAITTTGAACCAATGCTTCTTCCIAATGACAATACCGCTGTTCTGCAAAATTTTCAG	CAITTTGAACCAATGCTTCTTCCIAATGACAATACCGCTGTTCTGCAAAATTTTCAG	CAITTTGAACCAATGCTTCTTCCIAATGACAATACCGCTGTTCTGCAAAATTTTCAG	CAITTTGAACCAATGCTTCTTCCIAATGACAATACCGCTGTTCTGCAAAATTTTCAG

QY . 361 TCTAATCTCATTGAAAGCCACTCAACAACCTCTTTATGTGACAGATG 406

Db 412 TCTAATCTCATTTGAAAGCCACTCAACAACTCTTTATGTGACAGGTG 457

RESULT 3  
US-09-369-247-58  
; Sequence 58, Application US/09369247  
; Patent No. 6569992  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 44 Human Secreted Proteins  
; FILE REFERENCE: P2024P1  
; CURRENT APPLICATION NUMBER: US/09/369,247

Query Match 43.4%; Score 378; DB 3; Length 1940;  
Best Local Similarity 98.5%; Pred. No. 7.5e-103;  
Matches 400; Conservative 2; Mismatches 2; Indels 2; Gaps 2;

61 CCATATCTGGACATCTGGAAACATCCATGGGAAGAATCATGTGATGTACAGCTTTATATA 120  
|||  
141 CCATATCTGGACATCTGGAAACATCCATGGGAAGAATCATGTGATGTACAGCTTTATATA 200

121 AAGAGACAACTCTGAAACACTCCATCTTTAGCAGGAGATCCCTTTGAACTAGAAATGCCCTGTG 180  
201 AAGAGACAACTCTGAAACACTCCATCTTTAGCAGGAGATCCCTTTGAACTAGAAATGCCCTGTG 260

181 AAATACGTGTCTAAACAGCCCTCATGTGACTTGGTGAAGTCTCAATGGAAACAACATGTGTA 240  
|||||  
261 AAATACGTGTCTAAACAGCCCTCATGTGACTTGGTGAAGTCTCAATGGAAACAACATGTGTA 320  
|||||

241 AAACCTTGAAGATAGACAAACAAGTTGGAGGAAGAAGAACATTTTCATTTTTCATTTCA 300  
|||||  
321 AAACCTTGAAGATAGACAAACAAGTTGGAA-GAAGAGAAGAACATTTTCATTTTTCATTTCA 378

379 CRYTTTGAACCAAGTGTCTCTTAATGACAATGGGTGATACCGCTGTTCTGCAATAATTTTCAG 438

439 TCTAATCTCATTTGAAAGGCCACTCAACACTCTTTATGTGACAGGTG 484

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 10, 2006, 05:42:18 ; Search time 1394 Seconds  
(without alignments)  
561.171 Million cell updates/sec

Title: US-10-600-997-7  
Perfect score: 870  
Sequence: 1 atgaagacattgcctgcat.....ccatattgtgaggagttaa 870

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 6240305 seqs, 449581930 residues

Total number of hits satisfying chosen parameters: 12480610

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA\_New.\*  
1: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*  
2: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*  
3: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*  
4: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*  
5: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*  
6: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*  
7: /cgn2\_6/ptodata/1/pubpna/US12\_NEW\_PUB.seq.\*  
8: /cgn2\_6/ptodata/1/pubpna/US13\_NEW\_PUB.seq.\*  
9: /cgn2\_6/ptodata/1/pubpna/US14\_NEW\_PUB.seq.\*  
10: /cgn2\_6/ptodata/1/pubpna/US15\_NEW\_PUB.seq.\*  
11: /cgn2\_6/ptodata/1/pubpna/US16\_NEW\_PUB.seq.\*  
12: /cgn2\_6/ptodata/1/pubpna/US17\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	854	98.2	1066	7	US-10-987-663-1
2	829.2	95.3	888	7	US-10-987-663-9
3	564	64.8	726	7	US-10-987-663-7
4	36.8	4.2	1923	7	US-10-750-185-43526
5	36.8	4.2	1923	7	US-10-750-185-43526
6	36.8	4.2	147700	7	US-10-857-780-3
7	35.6	4.1	598	7	US-10-750-185-3972
8	35.6	4.1	598	7	US-10-750-185-3972
9	35.4	4.1	2902	7	US-10-793-626-3489
10	35	4.0	2884	7	US-10-750-185-27365
11	35	4.0	2884	7	US-10-750-185-27365
12	34.4	4.0	611587	11	US-11-117-187-209
13	34.2	3.9	1151	7	US-10-750-185-38526
14	34.2	3.9	1151	7	US-10-750-185-38526
15	34.2	3.9	1980	7	US-10-750-185-29535
16	34.2	3.9	1980	7	US-10-750-185-29535
17	34.2	3.9	1457619	11	US-11-098-686-8739
18	33.8	3.9	585	11	US-11-136-527-40
19	33.8	3.9	585	11	US-11-136-527-40
20	33.6	3.9	1217	7	US-10-750-185-41654
21	33.6	3.9	1217	7	US-10-750-185-41654

c	22	33.6	3.9	1402	7	US-10-750-185-38574	Sequence 38574, A
c	23	33.6	3.9	1402	7	US-10-750-623-38574	Sequence 38574, A
c	24	33.6	3.9	3001	11	US-11-145-703-133	Sequence 133, App
c	25	33.6	3.9	5439	7	US-10-750-185-63066	Sequence 63066, A
c	26	33.6	3.9	5439	7	US-10-750-623-63066	Sequence 63066, A
c	27	33.6	3.9	165627	11	US-11-121-086-89	Sequence 89, Appl
c	28	33.2	3.8	1589	7	US-10-750-185-35617	Sequence 35617, A
c	29	33.2	3.8	1589	7	US-10-750-623-35617	Sequence 35617, A
c	30	33	3.8	1400	11	US-11-136-527-7444	Sequence 7444, Ap
c	31	33	3.8	1692	11	US-11-136-527-3348	Sequence 3348, Ap
c	32	33	3.8	6113	7	US-10-240-708-14	Sequence 14, Appl
c	33	33	3.8	7872	11	US-11-136-527-23235	Sequence 23235, Ap
c	34	33	3.8	340000	11	US-11-102-978-3	Sequence 3, Appl1
c	35	32.8	3.8	159138	7	US-10-995-561-13230	Sequence 13230, A
c	36	32.6	3.7	949	7	US-10-750-185-34489	Sequence 34489, A
c	37	32.6	3.7	949	7	US-10-750-623-34489	Sequence 34489, A
c	38	32.6	3.7	952	7	US-10-750-185-28945	Sequence 28945, A
c	39	32.6	3.7	952	7	US-10-750-623-28945	Sequence 28945, A
c	40	32.4	3.7	1941	7	US-10-750-185-26450	Sequence 26450, A
c	41	32.4	3.7	1941	7	US-10-750-623-26450	Sequence 26450, A
c	42	32.4	3.7	2467	7	US-10-750-185-29248	Sequence 29248, A
c	43	32.4	3.7	2467	7	US-10-750-623-29248	Sequence 29248, A
c	44	32.4	3.7	188056	11	US-11-120-925-1	Sequence 1, Appl1
c	45	32.2	3.7	201	7	US-10-995-561-6891	Sequence 6891, Ap

## ALIGNMENTS

RESULT 1  
US-10-987-663-1  
; Sequence 1, Application US/10987663  
; Publication No. US20050272118A1  
; GENERAL INFORMATION:  
; APPLICANT: GENENTECH, INC.  
; APPLICANT: CLARK, HILARY  
; APPLICANT: EATON, DANIEL L.  
; APPLICANT: WRANIK, BERND  
; APPLICANT: OUYANG, WENJUN  
; APPLICANT: GONZALES, LINO  
; APPLICANT: LOYET, KELLY M.  
; TITLE OF INVENTION: Novel Compositions and Methods for the Treatment of  
; TITLE OF INVENTION: Immune Related Diseases  
; FILE REFERENCE: P1996RIP1-US  
; CURRENT APPLICATION NUMBER: US/10/987,663  
; CURRENT FILING DATE: 2004-11-12  
; PRIOR APPLICATION NUMBER: US 60/421,236  
; PRIOR FILING DATE: 2002-10-25  
; PRIOR APPLICATION NUMBER: US 10/371,341  
; PRIOR FILING DATE: 2003-02-19  
; NUMBER OF SEQ ID NOS: 10  
; SEQ ID NO 1  
; LENGTH: 1066  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-987-663-1

Query Match 98.2%; Score 854; DB 7; Length 1066;  
Best Local Similarity 98.9%; Pred. No. 4.5e-233;  
Matches 860; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY	1	ATGAAGACATTCGCTGCCATGCTTGGAACTGGGAATATTTTGGGTCTTCTTTAATC	60
DB	24	ATGAAGACATTCGCTGCCATGCTTGGAACTGGGAATATTTTGGGTCTTCTTTAATC	83
QY	61	CCATATCTGGACATCTGGAACTCCATGGGAAAGAAATCATGTGATGATACAGCTTTATATA	120
DB	84	CCATATCTGGACATCTGGAACTCCATGGGAAAGAAATCATGTGATGATACAGCTTTATATA	143
QY	121	AGAGACAATCTGAACATCTCCATCTTAGCAGAGATCCCTTTGAACATAGATGCCCTGTG	180
DB	144	AGAGACAATCTGAACATCTCCATCTTAGCAGAGATCCCTTTGAACATAGATGCCCTGTG	203







GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 10, 2006, 05:30:15 ; Search time 3747 Seconds  
(without alignments)  
10863.294 Million cell updates/sec

Title: US-10-600-997-7

Perfect score: 870

Sequence: 1 atgaagacattgcctgccat.....ccatattgtgaggagttaa 870

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST.\*  
1: gb\_est1.\*  
2: gb\_est2.\*  
3: gb\_est3.\*  
4: gb\_hic.\*  
5: gb\_est4.\*  
6: gb\_est5.\*  
7: gb\_est6.\*  
8: gb\_est7.\*  
9: gb\_gsa1.\*  
10: gb\_gsa2.\*  
11: gb\_gsa3.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	469.6	54.0	483	5	EX111230 EX111230
2	396.6	45.6	646	6	CD702861 EST19466
3	319.4	36.7	572	1	AW294080 UI-H-BI2
4	314.4	36.1	488	1	AI792952 om87f10.Y
5	289.6	33.3	478	1	AI651719 wb26a04.X
6	270.6	31.1	3229	4	AK041334 Mus muscu
7	257.2	29.6	444	1	AW188302 xj95a02.X
8	256.2	29.4	443	1	AW241471 xm59c06.X
9	254	29.2	445	2	BF940033 nac66d08
10	242.8	27.9	428	1	AW241411 xm58c06.X
11	185	21.3	763	7	CO558897 AGENCOURT
12	156.2	18.0	693	2	BB638002 BB638002
13	155.6	17.9	517	7	CN680177 E0133H03
14	138.8	16.0	633	2	BE306748 601104228
15	136	15.6	311	1	AA931122 om87f10.8
16	131.6	15.1	611	7	CO571762 AGENCOURT
17	126.8	14.6	855	9	BZ102470 CH230-237
18	123.4	14.2	599	11	CR049292 Forward 8
19	118.8	13.7	478	1	AI235902 EST32464
20	111.8	12.9	502	2	BF661404 maa85g11
21	91.2	10.5	396	7	CR474407 CR474407
22	72	8.3	748	6	CB963019 AGENCOURT

23	64.2	7.4	153	2	BE832323	BE832323 PMO-MT010
24	58	6.7	570	11	CR865259	CR865259 Sus acrofi
25	57	6.6	815	9	BZ273233	BZ273233 CH230-316
26	51.6	5.9	551	10	CG991478	CG991478 CH240_150
27	45.4	5.2	4756	4	CR857077	CR857077 Pongo pyg
28	42	4.8	777	9	BZ080723	BZ080723 11c05c04
29	40.6	4.7	423	8	T09379	T09379 EST07272 In
30	40.6	4.7	460	1	AI632280	AI632280 tt22b02.X
31	40.6	4.7	461	1	AI654788	AI654788 wb49g09.X
32	40.6	4.7	473	1	AI204353	AI204353 qf58g02.X
33	40.6	4.7	500	3	BM150540	BM150540 TCAPAD10
34	40.6	4.7	500	3	BM782571	BM782571 K-EST0059
35	40.6	4.7	501	6	CB135481	CB135481 K-EST0187
36	40.6	4.7	504	2	BF195894	BF195894 7c87a06.X
37	40.6	4.7	522	1	AI961504	AI961504 wt23f02.X
38	40.6	4.7	542	3	BI966027	BI966027 i872b03.X
39	40.6	4.7	549	2	BE348610	BE348610 hc72f11.X
40	40.6	4.7	549	6	CA868466	CA868466 1f80a05.X
41	40.6	4.7	573	2	BF111119	BF111119 7n43g09.X
42	40.6	4.7	579	3	BM829805	BM829805 K-EST0102
43	40.6	4.7	580	3	BM021328	BM021328 i875g06.Y
44	40.6	4.7	586	1	AI829721	AI829721 wt09f10.X
45	40.6	4.7	587	3	BM021090	BM021090 i875g06.X

#### ALIGNMENTS

RESULT 1  
EX111230  
LOCUS  
DEFINITION  
EX111230 NCI CGAP GC6 Homo sapiens cDNA clone IMAGp9981075716 ;  
IMAGE:2306766, mRNA sequence.  
ACCESSION  
EX111230.1 GI:27836886  
VERSION  
EST.  
KEYWORDS  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
REFERENCE  
1 (bases 1 to 483)  
AUTHORS  
Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,  
Radelof,U., Schneider,D. and Korn,B.  
TITLE  
Human Unigeneset - RZPD3  
JOURNAL  
Unpublished (2003)  
COMMENT  
Contact: Ina Rolfs  
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany  
RZPD; IMAGp9981075716.  
RZPDLIB, I.M.A.G.E. cDNA Clone Collection;  
Human Unigeneset - RZPD3 (RZPDLIB No.972)  
http://www.rzpd.de/CloneCards/cgi-  
bin/showLib.pl.cgi?response?libNo=972 Contact: Ina Rolfs  
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
Heubnerweg 6, D-14059 Berlin, Germany  
Tel: +49 30 32639 101  
Fax: +49 30 32639 111  
www.rzpd.de  
This clone is available royalty-free from RZPD;  
contact RZPD (clone@rzpd.de) for further information. Seq primer:  
M13r, Primer sequence: TTTCACACGGAACAGCTATGAC.  
FEATURES  
Location/Qualifiers  
1..483  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGp9981075716 ; IMAGE:2306766"  
/tissue\_type="pooled germ cell tumors"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP GC6"  
/note="Vector: pTT3D-Pac (Pharmacia) with a modified  
polylinker; Site\_1: Not I; Site\_2: Eco RI; Plasmid DNA



GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 8, 2006, 16:43:11 ; Search time 143 Seconds  
(without alignments)  
887.975 Million cell updates/sec

Title: US-10-600-997-8

Perfect score: 1557

Sequence: 1 MKTLPAMLTGKGLFWFFLI.....RLRNKKEAPTEYASICVRS 289

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_21.\*

1: Geneseqp1980s.\*

2: Geneseqp1990s.\*

3: Geneseqp2000s.\*

4: Geneseqp2001s.\*

5: Geneseqp2002s.\*

6: Geneseqp2003as.\*

7: Geneseqp2003bs.\*

8: Geneseqp2004s.\*

9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1557	100.0	289	ADH34662	Adh34662 Human BTL
2	1516	97.4	289	ADH34661	Adh34661 Human BTL
3	1516	97.4	289	ADH34661	Adh34661 Human BTL
4	1516	97.4	289	ADH34661	Adh34661 Human BTL
5	1516	97.4	289	ADH34661	Adh34661 Human BTL
6	1516	97.4	289	ADH34661	Adh34661 Human BTL
7	1516	97.4	289	ADH34661	Adh34661 Human BTL
8	1509	96.9	289	ADH34661	Adh34661 Human BTL
9	1479	95.0	283	ADH34661	Adh34661 Human BTL
10	1347	86.5	259	ADH34661	Adh34661 Human BTL
11	1246	80.0	239	ADH34661	Adh34661 Human BTL
12	1239	79.6	241	ADH34661	Adh34661 Human BTL
13	1239	79.6	241	ADH34661	Adh34661 Human BTL
14	981	63.0	194	ADH34661	Adh34661 Human BTL
15	958	61.5	178	ADH34661	Adh34661 Human BTL
16	849	54.5	157	ADH34661	Adh34661 Human BTL
17	819	52.6	390	ADH34661	Adh34661 Human BTL
18	789	50.7	148	ADH34661	Adh34661 Human BTL
19	741.5	47.6	212	ADH34661	Adh34661 Human BTL
20	741.5	47.6	212	ADH34661	Adh34661 Human BTL
21	741.5	47.6	212	ADH34661	Adh34661 Human BTL
22	723.5	46.5	306	ADH34661	Adh34661 Human BTL
23	719.5	46.2	306	ADH34661	Adh34661 Human BTL
24	719.5	46.2	538	ADH34661	Adh34661 Human BTL

25	680	43.7	127	8	ADU51061	ADU51061 Human SP
26	667	42.8	132	8	ADU51067	ADU51067 Human SP
27	653.5	42.0	277	8	ADU51111	ADU51111 Murine SP
28	615.5	39.5	250	8	ADU51110	ADU51110 Murine SP
29	558	35.8	111	8	ADU51066	ADU51066 Human SP
30	540	34.7	98	9	AE92075	AE92075 Human BTL
31	516	33.1	101	6	ADA57590	ADA57590 Human sec
32	516	33.1	101	6	ADA57590	ADA57590 Human sec
33	516	33.1	101	6	ADA57590	ADA57590 Human sec
34	458	29.4	204	2	AAV30859	AAV30859 Human sec
35	440	28.3	78	3	AAV30859	AAV30859 Human sec
36	405	26.0	179	8	ADU51134	ADU51134 Murine SP
37	405	26.0	411	8	ADU51149	ADU51149 Spleen-ex
38	394	25.3	180	8	ADU51104	ADU51104 Murine SP
39	392	25.2	175	8	ADU51105	ADU51105 Murine SP
40	374	24.0	65	8	ADU51052	ADU51052 Human spl
41	341	21.9	67	8	ADU51065	ADU51065 Human SP
42	339	21.8	150	8	ADU51135	ADU51135 Murine SP
43	328	21.1	151	8	ADU51103	ADU51103 Murine SP
44	326	20.9	126	8	ADU51109	ADU51109 Murine SP
45	261.5	16.8	102	8	ADU51108	ADU51108 Murine sp

## ALIGNMENTS

RESULT 1  
ADH34662  
ID ADH34662 standard; protein; 289 AA.  
XX  
AC ADH34662;  
XX  
DT 11-MAR-2004 (first entry)  
XX  
DE Human BTLA.  
XX  
KW B7x; ligand; B and T lymphocyte attenuator; BTLA; tumour; inhibition;  
KW tumour-specific; immunological tolerance; cancer; autoimmune disease;  
KW diabetes; pre-eclampsia; rheumatoid arthritis; multiple sclerosis;  
KW infection; graft rejection; cell cycle progression; differentiation;  
KW survival; cytokine production; cytolytic activation;  
KW antigen presentation; antibody production.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..28  
FT Disulfide-bond 58..115 /note= "Signal peptide"  
FT Modified-site 110 /note= "Disulphide bond"  
FT Domain 154..182 /note= "Glycosylated"  
FT Region 223..229 /note= "Transmembrane domain"  
FT Region 254..262 /note= "Conserved sequence"  
FT Region 277..289 /note= "Conserved sequence"  
XX  
WO2004000221-A2.  
XX  
PD 31-DEC-2003.  
XX  
XX 20-JUN-2003; 2003WO-US019614.  
XX  
XX 20-JUN-2002; 2002US-0390653P.  
XX  
XX 06-JAN-2003; 2003US-0438593P.  
XX  
XX (REGC ) UNIV CALIFORNIA.  
XX  
XX (UNIW ) UNIV WASHINGTON.

PI Allison JP, Murphy KP, Watanabe N, Murphy TL, Yang J, Zang X;  
 XX WPI; 2004-082409/08.  
 XX New recombinant B and T lymphocyte attenuator (BTLA).  
 PT useful for modulating B and T lymphocyte activity, or for diagnosing and  
 PT treating cancer, autoimmune disease or infectious disease.  
 XX Claim 81; Fig 28; 121pp; English.  
 CC This sequence represents a human B and T lymphocyte attenuator (BTLA).  
 CC BTLA acts as a negative regulator of both B and T lymphocyte activity,  
 CC where signaling mediated by BTLA results in the inhibition of BTLA-  
 CC positive lymphocyte activity. In BTLA-positive T cells BTLA signalling  
 CC can inhibit TCR-induced T cell responses, such as cell cycle progression,  
 CC differentiation, survival, cytokine production and cytolytic activation.  
 CC In BTLA-positive B cells BTLA signalling can inhibit B cell antigen  
 CC receptor-induced B cell responses, such as cell cycle progression,  
 CC differentiation, survival, antigen presentation and antibody production.  
 CC B7x is a ligand for the recombinant BTLA of the invention. B7x is able to  
 CC negatively regulate B and T lymphocyte activity through its interaction  
 CC with BTLA, which inhibits both B and T cell responses. Therefore B7x  
 CC positive tumour tissue inhibits the activity of tumour-specific T cells.  
 CC B7x is also expressed on non-tumour non-lymphoid tissue, showing that the  
 CC B7x/BTLA interaction is a mechanism for maintaining immunological  
 CC tolerance. BTLA proteins and related nucleic acids are useful for  
 CC modulating B and T lymphocyte activity, for diagnosing and treating  
 CC cancer, autoimmune disease, e.g. diabetes, pre-eclampsia, rheumatoid  
 CC arthritis or multiple sclerosis, or infectious disease, or for preventing  
 CC acute and/or chronic graft rejection.  
 XX Sequence '289 AA;  
 SQ

Query Match 100.0%; Score 1557; DB 8; Length 289;  
 Best Local Similarity 100.0%; Pred. No. 5.2e-140;  
 Matches 289; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MKTLPAMLTGKLFVFFFLIPYLDIWNHKGSCDVLQYIKRQSEHSILAGDPFLECPV 60  
 DB 1 MKTLPAMLTGKLFVFFFLIPYLDIWNHKGSCDVLQYIKRQSEHSILAGDPFLECPV 60  
 QY 61 KYCANRPHVTWCKLNGTTCVKLEDROTWSKEKNISFFILHPEPMLPNDNGSYRCSANFQ 120  
 DB 61 KYCANRPHVTWCKLNGTTCVKLEDROTWSKEKNISFFILHPEPMLPNDNGSYRCSANFQ 120  
 QY 121 SNLIESHSYTLVTDVKGASRPSKDEVASRPMWLLYSLLPLGLPLITTTWFCCLRR 180  
 DB 121 SNLIESHSYTLVTDVKGASRPSKDEVASRPMWLLYSLLPLGLPLITTTWFCCLRR 180  
 QY 181 HQGQNELSDTAGREINLVDAHLKSEQTASTRONSQVLLSEAGIYDNDPDLCFRMOEGS 240  
 DB 181 HQGQNELSDTAGREINLVDAHLKSEQTASTRONSQVLLSEAGIYDNDPDLCFRMOEGS 240  
 QY 241 EVCNPNCLSENPGIYVIALNSHNSVIGLSRLARNVKEAPTEYASICVRS 289  
 DB 241 EVCNPNCLSENPGIYVIALNSHNSVIGLSRLARNVKEAPTEYASICVRS 289

RESULT 2  
 ADH34661  
 ID ADH34661 standard; protein; 289 AA.  
 XX ADH34661;  
 XX  
 DT 11-MAR-2004 (first entry)  
 XX Human BTLA.  
 XX B7x; ligand; B and T lymphocyte attenuator; BTLA; tumour; inhibition;  
 KW tumour-specific; immunological tolerance; cancer; autoimmune disease;  
 KW diabetes; pre-eclampsia; rheumatoid arthritis; multiple sclerosis;  
 KW infection; graft rejection; cell cycle progression; differentiation;  
 KW survival; cytokine production; cytolytic activation;

KW antigen presentation; antibody production.  
 XX Homo sapiens.  
 XX Key Location/Qualifiers  
 FH Peptide 1..28  
 FT /note= "Signal peptide"  
 FT Disulfide-bond 58..115  
 FT /note = Disulphide bond  
 FT Modified-site 110  
 FT /note= "Glycosylated"  
 FT Domain 154..182  
 FT /note = Transmembrane domain  
 FT Region 223..229  
 FT /note= "Conserved sequence"  
 FT Region 254..262  
 FT /note= "Conserved sequence"  
 FT Region 277..289  
 FT /note= "Conserved sequence"  
 PN WO2004000221-A2.  
 XX 31-DEC-2003.  
 XX 20-JUN-2003; 2003WO-US019614.  
 XX 20-JUN-2003; 2002US-0390653P.  
 PR 06-JAN-2003; 2003US-0438593P.  
 XX (REGC ) UNIV CALIFORNIA.  
 XX (UNIW ) UNIV WASHINGTON.  
 PI Allison JP, Murphy KP, Watanabe N, Murphy TL, Yang J, Zang X;  
 XX WPI; 2004-082409/08.  
 XX New recombinant B and T lymphocyte attenuator nucleic acid and protein,  
 PT useful for modulating B and T lymphocyte activity, or for diagnosing and  
 PT treating cancer, autoimmune disease or infectious disease.  
 XX Example 4; Fig 19; 121pp; English.  
 CC This sequence represents a human B and T lymphocyte attenuator (BTLA).  
 CC BTLA acts as a negative regulator of both B and T lymphocyte activity,  
 CC where signaling mediated by BTLA results in the inhibition of BTLA-  
 CC positive lymphocyte activity. In BTLA-positive T cells BTLA signalling  
 CC can inhibit TCR-induced T cell responses, such as cell cycle progression,  
 CC differentiation, survival, cytokine production and cytolytic activation.  
 CC In BTLA-positive B cells BTLA signalling can inhibit B cell antigen  
 CC receptor-induced B cell responses, such as cell cycle progression,  
 CC differentiation, survival, antigen presentation and antibody production.  
 CC B7x is a ligand for the recombinant BTLA of the invention. B7x is able to  
 CC negatively regulate B and T lymphocyte activity through its interaction  
 CC with BTLA, which inhibits both B and T cell responses. Therefore B7x  
 CC positive tumour tissue inhibits the activity of tumour-specific T cells.  
 CC B7x is also expressed on non-tumour non-lymphoid tissue, showing that the  
 CC B7x/BTLA interaction is a mechanism for maintaining immunological  
 CC tolerance. BTLA proteins and related nucleic acids are useful for  
 CC modulating B and T lymphocyte activity, for diagnosing and treating  
 CC cancer, autoimmune disease, e.g. diabetes, pre-eclampsia, rheumatoid  
 CC arthritis or multiple sclerosis, or infectious disease, or for preventing  
 CC acute and/or chronic graft rejection.  
 XX Sequence 289 AA;  
 SQ

Query Match 97.4%; Score 1516; DB 8; Length 289;  
 Best Local Similarity 97.9%; Pred. No. 4.3e-136;  
 Matches 283; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 MKTLPAMLTGKLFVFFFLIPYLDIWNHKGSCDVLQYIKRQSEHSILAGDPFLECPV 60  
 DB 1 MKTLPAMLTGKLFVFFFLIPYLDIWNHKGSCDVLQYIKRQSEHSILAGDPFLECPV 60

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 8, 2006, 16:54:56 ; Search time 118.5 Seconds  
(without alignments)  
1019.010 Million cell updates/sec

Title: US-10-600-997-8  
Perfect score: 1557  
Sequence: 1 MKTLPAMLGKGLFWFFLI.....RLARNVKEAPTEYASICVRS 289

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA\_Main:  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1557	100.0	289	4	US-10-600-997-8
2	1516	97.4	289	4	US-10-371-341-2
3	1516	97.4	289	4	US-10-600-997-6
4	1516	97.4	289	5	US-10-831-622-21
5	1516	97.4	289	5	US-10-964-215-21
6	1516	97.4	289	5	US-10-989-826-28
7	1516	97.4	521	5	US-10-831-622-98
8	1516	97.4	521	5	US-10-964-215-98
9	1347	86.5	259	5	US-10-831-622-20
10	1347	86.5	259	5	US-10-964-215-20
11	1246	80.0	239	5	US-10-831-622-19
12	1246	80.0	239	5	US-10-964-215-19
13	1239	79.6	241	4	US-10-471-449-10
14	958	61.5	178	5	US-10-831-622-15
15	958	61.5	178	5	US-10-964-215-15
16	849	54.5	157	5	US-10-831-622-13
17	849	54.5	157	5	US-10-964-215-13
18	789	50.7	148	5	US-10-831-622-14
19	789	50.7	148	5	US-10-964-215-14
20	741.5	47.6	212	4	US-10-062-548-88
21	741.5	47.6	212	5	US-10-918-446-88
22	741.5	47.6	212	6	US-11-002-755-88
23	741.5	47.6	212	6	US-11-002-756-88
24	723.5	46.5	306	4	US-10-600-997-5
25	723.5	46.5	306	4	US-10-600-997-10
26	719.5	46.2	306	5	US-10-831-622-63
27	719.5	46.2	306	5	US-10-964-215-63

ALIGNMENTS

RESULT 1

US-10-600-997-8  
; Sequence 8, Application US/10600997  
; Publication No. US20040175380A1  
; GENERAL INFORMATION:  
; APPLICANT: Allison, James  
; APPLICANT: Murphy, Kenneth  
; APPLICANT: Watanabe, Norihiko  
; APPLICANT: Murphy, Theresa  
; APPLICANT: Yang, Jianfei  
; APPLICANT: Zang, Xingxing  
; TITLE OF INVENTION: Compositions and Methods for Modulating Lymphocyte Activity  
; FILE REFERENCE: A-71608/TAL/DHR  
; CURRENT APPLICATION NUMBER: US/10/600,997  
; CURRENT FILING DATE: 2003-06-20  
; PRIOR APPLICATION NUMBER: US 60/390,653  
; PRIOR FILING DATE: 2002-06-20  
; PRIOR APPLICATION NUMBER: US 60/438,593  
; PRIOR FILING DATE: 2003-01-06  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 8  
; LENGTH: 289  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-600-997-8

Query Match 100.0%; Score 1557; DB 4; Length 289;  
Best Local Similarity 100.0%; Pred. No. 1e-149; Mismatches 0; Indels 0; Gaps 0;

Percent Similarity 100.0%; Read: NO. 12-143;				
Matches 289; Conservative 0; Mismatches 0; Indels 0; Gaps 0				
Qy	1	MKTLPAMLGKGLFWFFFLI	PYLDIWNTHGKSCDVQLYIKRQSEHSILAGDPFLECPV	60
Db	1	MKTLPAMLGKGLFWFFFLI	PYLDIWNTHGKSCDVQLYIKRQSEHSILAGDPFLECPV	60
Qy	61	KYCANRPHVTWCKLNGTTCVKLEDRQTSWKEKNISPFILHPEPMLPNDNGSYRCSANFQ	120	
Db	61	KYCANRPHVTWCKLNGTTCVKLEDRQTSWKEKNISPFILHPEPMLPNDNGSYRCSANFQ	120	
Qy	121	SNLTESHSTTLYVTDVKGASRPSKDEVASRPMLLYSLLPLGGGLPLTTWFCFLCRR	180	
Db	121	SNLTESHSTTLYVTDVKGASRPSKDEVASRPMLLYSLLPLGGGLPLTTWFCFLCRR	180	
Qy	181	HQGNQNELSTAGREINLVDAHLKSEOTEASTRONSOVLLSEAGIYDNDPDLCFRMOEGS	240	
Db	181	HQGNQNELSTAGREINLVDAHLKSEOTEASTRONSOVLLSEAGIYDNDPDLCFRMOEGS	240	
Qy	241	EVCNSPCLEENKPGIVYASLNHVSIGLNSRLARNVKEAPTEYASICVRS	289	
Db	241	EVCNSPCLEENKPGIVYASLNHVSIGLNSRLARNVKEAPTEYASICVRS	289	



GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 8, 2006, 16:54:06 ; Search time 34.5 Seconds  
(without alignments)  
692.559 Million cell updates/sec

Title: US-10-600-997-8  
Perfect score: 1557  
Sequence: 1 MKTLPAMLTGKLFVFFLI.....RLARNVKEAPTEYASICVRS 289

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2.6/prodata/1/iaa/5 COMB.pep.\*  
2: /cgn2.6/prodata/1/iaa/6 COMB.pep.\*  
3: /cgn2.6/prodata/1/iaa/H COMB.pep.\*  
4: /cgn2.6/prodata/1/iaa/PCTUS COMB.pep.\*  
5: /cgn2.6/prodata/1/iaa/RE COMB.pep.\*  
6: /cgn2.6/prodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	741.5	47.6	212	2	US-09-369-247-88
2	741.5	47.6	212	2	US-10-062-548-88
3	516	33.1	102	2	US-09-369-247-107
4	516	33.1	102	2	US-10-062-548-107
5	440	28.3	78	2	US-09-513-999C-7032
6	121.5	7.8	343	1	US-08-348-792-10
7	121.5	7.8	343	1	US-08-462-738-10
8	121.5	7.8	343	2	US-09-199-955-10
9	121.5	7.8	343	2	US-08-880-875-10
10	117	7.5	1953	2	US-09-917-254-92
11	115	7.4	624	1	US-08-642-406A-22
12	115	7.4	624	2	US-09-199-534-22
13	115	7.4	624	2	US-09-199-534-22
14	115	7.4	624	2	US-09-491-322-22
15	115	7.4	773	2	US-08-434-000A-2
16	115	7.4	773	2	US-09-312-157-2
17	115	7.4	773	2	US-09-717-888-2
18	115	7.4	773	2	US-09-818-247-6
19	101.5	6.5	329	1	US-08-348-792-12
20	101.5	6.5	329	1	US-08-462-738-12
21	101.5	6.5	329	2	US-09-199-955-12
22	101.5	6.5	329	2	US-08-880-875-12
23	98.5	6.3	278	2	US-09-270-767-42034
24	97.5	6.3	119	2	US-09-858-664A-30
25	97.5	6.3	119	2	US-10-274-978-31
26	97.5	6.3	119	2	US-10-697-263-31
27	97.5	6.3	766	2	US-09-854-845-49

28	97.5	6.3	771	2	US-09-854-845-47	Sequence 47, Appl
29	97.5	6.3	865	2	US-09-854-845-33	Sequence 33, Appl
30	97.5	6.3	870	2	US-09-854-845-31	Sequence 31, Appl
31	95.5	6.1	739	2	US-09-854-845-45	Sequence 45, Appl
32	95.5	6.1	744	2	US-09-854-845-43	Sequence 43, Appl
33	95.5	6.1	838	2	US-09-854-845-29	Sequence 29, Appl
34	95.5	6.1	843	2	US-09-854-845-27	Sequence 27, Appl
35	94	6.0	771	1	US-08-742-753-2	Sequence 2, Appl
36	93.5	6.0	622	2	US-09-499-846-2	Sequence 8, Appl
37	93	6.0	921	1	US-08-568-459A-8	Sequence 8, Appl
38	93	6.0	921	1	US-08-487-826B-8	Sequence 8, Appl
39	93	6.0	921	2	US-09-210-288-8	Sequence 8, Appl
40	93	6.0	921	2	US-10-153-273-8	Sequence 8, Appl
41	90.5	5.8	283	2	US-09-904-615-106	Sequence 106, App
42	90.5	5.8	283	2	US-10-054-988-106	Sequence 106, App
43	90	5.8	780	1	US-08-232-538-14	Sequence 14, Appl
44	90	5.8	780	1	US-08-786-164-14	Sequence 14, Appl
45	90	5.8	1311	1	US-08-340-011-5	Sequence 5, Appl

## ALIGNMENTS

## RESULT 1

US-09-369-247-88  
; Sequence 88, Application US/09369247  
; Patent No. 6569992  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 44 Human Secreted Proteins  
; FILE REFERENCE: P2024P1  
; CURRENT APPLICATION NUMBER: US/09/369,247  
; CURRENT FILING DATE: 1999-08-05  
; EARLIER APPLICATION NUMBER: 60/074,118  
; EARLIER FILING DATE: 1998-02-09  
; EARLIER APPLICATION NUMBER: 60/074,157  
; EARLIER FILING DATE: 1998-02-09  
; EARLIER APPLICATION NUMBER: 60/074,137  
; EARLIER FILING DATE: 1998-02-09  
; EARLIER APPLICATION NUMBER: 60/074,341  
; EARLIER FILING DATE: 1998-02-09  
; EARLIER APPLICATION NUMBER: 60/074,141  
; EARLIER FILING DATE: 1998-02-09  
; NUMBER OF SEQ ID NOS: 172  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 88  
; LENGTH: 212  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-369-247-88

Query Match 47.6%; Score 741.5; DB 2; Length 212;

Best Local Similarity 94.4%; Pred. No. 3.4e-69;  
Matches 136; Conservative 4; Mismatches 3; Indels 1; Gaps 1;

QY	1	MKTLPAMLTGKLFVFFLI	PYLDIWNHGKSCDQVLYIKQSEHSILAGDPFELECPV	60
DB	1	MKTLPAMLTGKLFVFFLI	PYLDIWNHGKSCDQVLYIKQSEHSILAGDPFELECPV	60
QY	61	KYCANRPHVTVCKLNGTTTCVKLEDQTSWKEKNISFFILHPEPMLPNDNGSYRCSANFQ	120	
DB	61	KYCANRPHVTVCKLNGTTTCVKLEDQTSWKEKNISFFILHPEPMLPNDNGSYRCSANFQ	120	
QY	121	SNLIESHTTLYVTVKGSERPS	144	
DB	121	SNLIESHTTLYVTG-EFSTPRPS	143	

## RESULT 2

US-10-062-548-88  
; Sequence 88, Application US/10062548  
; Patent No. 6924356  
; GENERAL INFORMATION:



```
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 44 Human Secreted Proteins
; FILE REFERENCE: P2024PI
; CURRENT APPLICATION NUMBER: US/10/062,548
; PRIOR FILING DATE: 2002-02-05
; PRIOR FILING DATE: 1999-08-05
; PRIOR FILING DATE: 1999-08-05
; PRIOR FILING DATE: 1998-02-09
; PRIOR FILING DATE: 1998-02-09
; PRIOR FILING DATE: 1998-02-09
; PRIOR FILING DATE: 1998-02-09
; PRIOR FILING DATE: 1998-02-09
; PRIOR FILING DATE: 1998-02-09
; PRIOR FILING DATE: 1998-02-09
; PRIOR FILING DATE: 1998-02-09
; PRIOR FILING DATE: 1998-02-09
; PRIOR FILING DATE: 1998-02-09
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 88
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
; GENERAL INFORMATION:
US-10-062-548-88

Query Match      47.6%; Score 741.5; DB 2; Length 212;
Best Local Similarity 94.4%; Pred. NO. 3.4e-69;
Matches 136; Conservative 4; Mismatches 3; Indels 1; Gaps 1;

QY 1 M K T L P A M L G T G K L F W V F F L I P Y L D I W N I H G K S C D V Q L Y I K R Q S H S I L A G D P F F L E C P V 60
D b 1 M K T L P A M L G T G K L F W V F F L I P Y L D I W N I H G K S C D V Q L Y I K R Q S H S I L A G D P F F L E C P V 60
QY 61 K Y C A N R P H V T W C K L N G T T C V K L E D R Q T S W K E E K N I S F F I L H F E P M L P N D N G S Y R C S A N F Q 120
D b 61 K Y C A N R P H V T W C K L N G T T C V K L E D R Q T S W K E E K N I S F F I L H F E P M L P N D N G S Y R C S A N F Q 120
QY 121 S N L I E S H S T T L Y V T D V K G A S E R P S 144
D b 121 S N L I E S H S T T L Y V T G - E F S T P R P S 143

RESULT 3
US-09-369-247-107
; Sequence 107, Application US/09369247
; Patent No. 6569992
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 44 Human Secreted Proteins
; FILE REFERENCE: P2024PI
; CURRENT APPLICATION NUMBER: US/09/369,247
; CURRENT FILING DATE: 1999-08-05
; EARLIER APPLICATION NUMBER: 60/074,118
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,157
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,137
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,341
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,141
; EARLIER FILING DATE: 1998-02-09
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 107
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (101)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (102)
; OTHER INFORMATION: Xaa equals stop translation
US-10-062-548-107

Query Match      33.1%; Score 516; DB 2; Length 102;
Best Local Similarity 93.8%; Pred. NO. 4.2e-46;
Matches 91; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 M K T L P A M L G T G K L F W V F F L I P Y L D I W N I H G K S C D V Q L Y I K R Q S H S I L A G D P F F L E C P V 60
D b 1 M K T L P A M L G T G K L F W V F F L I P Y L D I W N I H G K S C D V Q L Y I K R Q S H S I L A G D P F F L E C P V 60
QY 61 K Y C A N R P H V T W C K L N G T T C V K L E D R Q T S W K E E K N I S F 97
D b 61 K Y C A N R P H V T W C K L N G T T C V K L E D R Q T S W K K R T P H F 97

RESULT 4
US-10-062-548-107
; Sequence 107, Application US/10062548
; Patent No. 6924356
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 44 Human Secreted Proteins
; FILE REFERENCE: P2024PI
; CURRENT APPLICATION NUMBER: US/10/062,548
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 09/369,247
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/074,118
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/074,157
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/074,137
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/074,341
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/074,141
; PRIOR FILING DATE: 1998-02-09
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 107
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (101)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (102)
; OTHER INFORMATION: Xaa equals stop translation
US-10-062-548-107

Query Match      33.1%; Score 516; DB 2; Length 102;
Best Local Similarity 93.8%; Pred. NO. 4.2e-46;
Matches 91; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 M K T L P A M L G T G K L F W V F F L I P Y L D I W N I H G K S C D V Q L Y I K R Q S H S I L A G D P F F L E C P V 60
D b 1 M K T L P A M L G T G K L F W V F F L I P Y L D I W N I H G K S C D V Q L Y I K R Q S H S I L A G D P F F L E C P V 60
QY 61 K Y C A N R P H V T W C K L N G T T C V K L E D R Q T S W K E E K N I S F 97
D b 61 K Y C A N R P H V T W C K L N G T T C V K L E D R Q T S W K K R T P H F 97

RESULT 5
US-09-513-999C-7032
; Sequence 7032, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
```

```
; NAME/KEY: SITE
; LOCATION: (102)
; OTHER INFORMATION: Xaa equals stop translation
US-09-369-247-107

Query Match      33.1%; Score 516; DB 2; Length 102;
Best Local Similarity 93.8%; Pred. NO. 4.2e-46;
Matches 91; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 M K T L P A M L G T G K L F W V F F L I P Y L D I W N I H G K S C D V Q L Y I K R Q S H S I L A G D P F F L E C P V 60
D b 1 M K T L P A M L G T G K L F W V F F L I P Y L D I W N I H G K S C D V Q L Y I K R Q S H S I L A G D P F F L E C P V 60
QY 61 K Y C A N R P H V T W C K L N G T T C V K L E D R Q T S W K E E K N I S F 97
D b 61 K Y C A N R P H V T W C K L N G T T C V K L E D R Q T S W K K R T P H F 97
```

```
RESULT 4
US-10-062-548-107
; Sequence 107, Application US/10062548
; Patent No. 6924356
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 44 Human Secreted Proteins
; FILE REFERENCE: P2024PI
; CURRENT APPLICATION NUMBER: US/10/062,548
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 09/369,247
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/074,118
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/074,157
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/074,137
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/074,341
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/074,141
; PRIOR FILING DATE: 1998-02-09
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 107
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (101)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (102)
; OTHER INFORMATION: Xaa equals stop translation
US-10-062-548-107
```

```
Query Match      33.1%; Score 516; DB 2; Length 102;
Best Local Similarity 93.8%; Pred. NO. 4.2e-46;
Matches 91; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 M K T L P A M L G T G K L F W V F F L I P Y L D I W N I H G K S C D V Q L Y I K R Q S H S I L A G D P F F L E C P V 60
D b 1 M K T L P A M L G T G K L F W V F F L I P Y L D I W N I H G K S C D V Q L Y I K R Q S H S I L A G D P F F L E C P V 60
QY 61 K Y C A N R P H V T W C K L N G T T C V K L E D R Q T S W K E E K N I S F 97
D b 61 K Y C A N R P H V T W C K L N G T T C V K L E D R Q T S W K K R T P H F 97
```

```
RESULT 5
US-09-513-999C-7032
; Sequence 7032, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
```

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	1516	97.4	289	6	US-10-987-663-2	Sequence 2, Appli
2	1503	96.5	295	6	US-10-987-663-10	Sequence 10, Appli
3	1239	79.6	241	6	US-10-987-663-8	Sequence 8, Appli
4	90.5	5.8	822	7	US-11-183-567A-2	Sequence 2, Appli
5	90	5.8	1338	7	US-11-109-156-23	Sequence 23, Appli
6	90	5.8	3588	6	US-10-995-561-672	Sequence 672, App
7	90	5.8	4346	6	US-10-995-561-671	Sequence 671, App
8	90	5.8	4347	6	US-10-995-561-670	Sequence 670, App
9	90	5.8	4390	7	US-11-169-041-169	Sequence 169, App
10	90	5.8	4419	6	US-10-821-234-1155	Sequence 1155, App
11	89	5.7	4495	6	US-10-453-372-1002	Sequence 1002, Ap
12	89	5.7	5636	7	US-11-065-695-20	Sequence 20, Appli
13	88	5.7	244	7	US-11-156-084-218	Sequence 218, App
14	87	5.6	2828	7	US-11-080-991-54	Sequence 54, Appli
15	87	5.6	2828	7	US-11-186-284-49	Sequence 49, Appli
16	86	5.5	1338	6	US-10-821-234-1622	Sequence 1622, Ap
17	85.5	5.5	976	7	US-11-148-770-31	Sequence 31, Appli
18	85.5	5.5	1150	7	US-11-139-435-1	Sequence 1, Appli
19	85	5.5	534	6	US-10-821-234-1341	Sequence 1341, Ap
20	84	5.4	235	6	US-10-453-372-784	Sequence 784, App
21	84	5.4	284	6	US-10-453-372-790	Sequence 790, App
22	84	5.4	290	6	US-10-453-372-776	Sequence 776, App
23	84	5.4	302	6	US-10-453-372-780	Sequence 780, App
24	84	5.4	302	6	US-10-453-372-782	Sequence 782, App
25	84	5.4	302	6	US-10-453-372-788	Sequence 788, App

```
QY 241 EYCSNPCLNKPGLVYASLNHSHVIGLNSRLARNVKEAPTEYASICVRS 289
|||
Db 241 EYVSNPCLNKPGLVYASLNHSHVIGLNSRLARNVKEAPTEYASICVRS 289
|||
RESULT 2
US-10-987-663-10
; Sequence 10, Application US/10987663
; Publication NO. US20050272118A1
; GENERAL INFORMATION:
; APPLICANT: GENENTECH, INC.
; APPLICANT: CLARK, HILARY L.
; APPLICANT: EATON, DANIEL L.
; APPLICANT: WRANIK, BERND
; APPLICANT: OUYANG, WENJUN
; APPLICANT: GONZALES, LINO
; APPLICANT: LOYET, KELLY M.
; TITLE OF INVENTION: Novel Compositions and Methods for the Treatment of
; TITLE OF INVENTION: Immune Related Diseases
; FILE REFERENCE: P1996R1P1-US
; CURRENT APPLICATION NUMBER: US/10/987,663
; PRIOR FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US 60/421,236
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 10/371,341
; PRIOR FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 10
; LENGTH: 295
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-987-663-10
Query Match 96.5%; Score 1503; DB 6; Length 295;
Best Local Similarity 95.9%; Pred. No. 1.3e-137;
Matches 283; Conservative 2; Mismatches 4; Indels 6; Gaps 1;

QY 1 MKTLPAMLTGKLFVWFPIIPYLDIWNHKGSCDVQLYIKRQSEHSILAGDPFPELECPV 60
|||
Db 1 MKTLPAMLTGKLFVWFPIIPYLDIWNHKGSCDVQLYIKRQSEHSILAGDPFPELECPV 60
|||
QY 61 KYCANRPHVTWCKLNGTTCVKLEDRQTSWKEKNISFFILHPEPMLPNDNGSYRCSANFQ 120
|||
Db 61 KYCANRPHVTWCKLNGTTCVKLEDRQTSWKEKNISFFILHPEPMLPNDNGSYRCSANFQ 120
|||
QY 121 SNLIESHTTLYVT-----DVKGASERSKDEVASRPMWLLYSLPLGGLPLLITTWFC 174
|||
Db 121 SNLIESHTTLYVTAFNTIPDVKSASERSKDEMASRPMWLLYSLPLGGLPLLITTCFCL 180
|||
QY 175 FCCLRRHQKQNELSDTAGREINLVDHLKSEQTEASTRQNSQVLLSEAGIYDNDPDLCF 234
|||
Db 181 FCCLRRHQKQNELSDTAGREINLVDHLKSEQTEASTRQNSQVLLSEAGIYDNDPDLCF 240
|||
QY 235 RMOGSEVSNPCLNKPGLVYASLNHSHVIGLNSRLARNVKEAPTEYASICVRS 289
|||
Db 241 RMOGSEVSNPCLNKPGLVYASLNHSHVIGLNSRLARNVKEAPTEYASICVRS 295
|||
RESULT 3
US-10-987-663-8
; Sequence 8, Application US/10987663
; Publication NO. US20050272118A1
; GENERAL INFORMATION:
; APPLICANT: GENENTECH, INC.
; APPLICANT: CLARK, HILARY L.
; APPLICANT: EATON, DANIEL L.
; APPLICANT: WRANIK, BERND
; APPLICANT: OUYANG, WENJUN
; APPLICANT: GONZALES, LINO
; APPLICANT: LOYET, KELLY M.
; TITLE OF INVENTION: Novel Compositions and Methods for the Treatment of
; TITLE OF INVENTION: Immune Related Diseases
; FILE REFERENCE: P1996R1P1-US
```

```
; CURRENT APPLICATION NUMBER: US/10/987,663
; CURRENT FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US 60/421,236
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 10/371,341
; PRIOR FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 8
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-987-663-8
Query Match 79.6%; Score 1239; DB 6; Length 241;
Best Local Similarity 82.4%; Pred. No. 2.9e-112;
Matches 238; Conservative 1; Mismatches 2; Indels 48; Gaps 1;

QY 1 MKTLPAMLTGKLFVWFPIIPYLDIWNHKGSCDVQLYIKRQSEHSILAGDPFPELECPV 60
|||
Db 1 MKTLPAMLTGKLFVWFPIIPYLDIWNHKGSCDVQLYIKRQSEHSILAGDPFPELECPV 60
|||
QY 61 KYCANRPHVTWCKLNGTTCVKLEDRQTSWKEKNISFFILHPEPMLPNDNGSYRCSANFQ 120
|||
Db 61 KYCANRPHVTWCKLNGTTCVKLEDRQTSWKEKNISFFILHPEPMLPNDNGSYRCSANFQ 120
|||
QY 121 SNLIESHTTLYVTVDKASERPSKDEVASRPMWLLYSLPLGGLPLLITTWFCCLRR 180
|||
Db 121 SNLIESHTTLYVT-----134
|||
QY 181 HOGKQNELSDTAGREINLVDHLKSEQTEASTRQNSQVLLSEAGIYDNDPDLCFRMOG 240
|||
Db 135 --GKQNELSDTAGREINLVDHLKSEQTEASTRQNSQVLLSETGYDNDPDLCFRMOG 192
|||
QY 241 EYCSNPCLNKPGLVYASLNHSHVIGLNSRLARNVKEAPTEYASICVRS 289
|||
Db 193 EYVSNPCLNKPGLVYASLNHSHVIGLNSRLARNVKEAPTEYASICVRS 241
|||
RESULT 4
US-11-183-567A-2
; Sequence 2, Application US/11183567A
; Publication NO. US20060019296A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Ming-Ming
; APPLICANT: Goldfarb, Mitchell
; TITLE OF INVENTION: Methods of Identifying Modulators of the
; TITLE OF INVENTION: FGF Receptor
; FILE REFERENCE: 2459-1-002NCON
; CURRENT APPLICATION NUMBER: US/11/183,567A
; CURRENT FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: 09/757,415
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/175,867
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 822
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-183-567A-2
Query Match 5.8%; Score 90.5; DB 7; Length 822;
Best Local Similarity 21.7%; Pred. No. 0.71;
Matches 69; Conservative 40; Mismatches 116; Indels 93; Gaps 17;

QY 27 NIHKGSCDVQLYIKRQSEH-----SILAGDPFPELECPKYCANRPHVTWCK- 73
|||
Db 234 NEYGSINHTYQLDVVVERSPHRPILQAGLPANETVGSNVFPMCKV-YSDPQPHIQLKH 292
|||
QY 74 --LNG-----TTCVKLEDRQTSWKEKNISFFILHPEPMLPNDNGSYRCS 116
|||
Db 293 IEVNGSKIGPDNLPVQILKTAGVNTDKEMEVLHRLNVSP-----EDAGEYTC 342
|||
```

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 8, 2006, 16:48:30 ; Search time 26.5 Seconds  
(without alignments)  
1049.307 Million cell updates/sec

Title: US-10-600-997-8

Perfect score: 1557

Sequence: 1 MKTLPAMLTGKLFVWFLLI.....RLARNVKEAPTEYASICVRS 289

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 80:\*

1: PIR1:\*

2: PIR2:\*

3: PIR3:\*

4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	115	7.4	773	1 QRRBG	secretory component
2	113.5	7.3	841	2 JCS894	killer cell inhibi
3	111	7.1	6642	2 T29757	protein UNC-89 - C
4	110	7.1	335	2 A53434	cell surface glyco
5	107	6.9	1852	2 A37860	calcium channel pr
6	104.5	6.7	1036	2 S22383	axonin 1 precursor
7	104.5	6.7	6805	2 S22901	titin - rabbit (fr
8	104	6.7	7962	2 I38346	elastic titin - hu
9	102.5	6.6	5175	2 T20992	hypothetical prote
10	102.5	6.6	5198	2 T43290	hemectin precurs
11	99.5	6.4	26926	1 I38344	titin, cardiac mus
12	98.5	6.3	480	2 A56182	fibroblast growth
13	98	6.3	1336	2 I60598	Fit-1 tyrosine kin
14	96.5	6.2	1158	2 S33901	reverse transcript
15	94.5	6.1	812	1 A36477	fibroblast growth
16	94	6.0	978	1 A49814	protein-tyrosine k
17	93	6.0	1277	2 T30532	neural cell adhesi
18	92	5.9	3707	2 S18252	heparan sulfate pr
19	91.5	5.9	210	2 S28557	T-cell surface gly
20	91.5	5.9	806	2 A35963	protein-tyrosine k
21	90.5	5.8	729	2 B56182	fibroblast growth
22	90.5	5.8	729	2 A56795	fibroblast growth
23	90.5	5.8	733	2 I49293	fibroblast growth
24	90.5	5.8	822	1 TVMSFG	fibroblast growth
25	90.5	5.8	822	2 I42889	fibroblast growth
26	90.5	5.8	832	2 JH0393	fibroblast growth
27	90.5	5.8	1209	2 T42718	probable neural ce
28	90	5.8	1338	2 S09982	protein-tyrosine k
29	90	5.8	4391	2 A38096	perlecan precursor

30	89.5	5.7	210	2 E46482	T-cell surface gly
31	89.5	5.7	221	2 C46482	T-cell surface gly
32	89.5	5.7	246	2 T01073	T cell surface gly
33	89.5	5.7	296	2 B53434	cell surface glyco
34	89.5	5.7	303	2 A40807	membrane glycoprot
35	89.5	5.7	570	2 A57535	interleukin 1 recep
36	89.5	5.7	814	1 A39752	fibroblast growth
37	89	5.7	214	2 A11073	probable membrane
38	88.5	5.7	152	2 I39464	CD8 antigen - huma
39	88	5.7	244	2 AD1834	isopentenyl transf
40	87.5	5.6	662	2 C40862	heparin-binding gr
41	87.5	5.6	818	2 JC4058	fibroblast growth
42	87.5	5.6	822	1 TVHUF8	fibroblast growth
43	87.5	5.6	822	2 S29840	fibroblast growth
44	87.5	5.6	1177	2 T16594	hypothetical prote
45	87.5	5.6	1323	2 PN0568	connectin 3B - Chi

#### ALIGNMENTS

##### RESULT 1

QRRBG

secretory component precursor - rabbit

N;Alternate names: poly-Ig receptor; polymeric immunoglobulin receptor

N;Contains: free secretory component; transmembrane secretory component

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 15-Nov-1984 #sequence\_revision 15-Nov-1984 #text\_change 09-Jul-2004

C;Accession: A02111; A28077

R;Mostov, K.E.; Friedlander, M.; Blobel, G.

Nature 308, 37-43, 1984

A;Title: The receptor for transepithelial transport of IgA and IGM contains multiple ir

A;Reference number: A02111; MUID:84142246; PMID:6322002

A;Accession: A02111

A;Molecule type: mRNA

A;Residues: 1-773 <MOS>

A;Cross-references: UNIPROT:P01832; UNIPARC:UPI000043E81; GB:X00412; GB:X01291; NID:gi

A;Note: the authors translated the codon ACC for residue 54 as Asn

R;Frutiger, S.; Hughes, G.J.; Hanly, W.C.; Jaton, J.C.

J. Biol. Chem. 263, 8120-8125, 1988

A;Title: Rabbit secretory components of different allotypes vary in their carbohydrate

A;Reference number: A28077; MUID:88228032; PMID:3131339

A;Accession: A28077

A;Molecule type: protein

A;Residues: 87-114;410-424 <FRU>

A;Cross-references: UNIPARC:UPI000017374B; UNIPARC:UPI000017374C

C;Comment: This receptor binds polymeric IgA and IGM at the basolateral surface of epit

process, cleavage occurs to separate the extracellular portion, also known as the secre

C;Comment: The five domains exhibit homology with immunoglobulin V regions. The similar

C;Comment: Alternative splicing in the extracellular domain leads to high or low molecu

C;Superfamily: secretory component; immunoglobulin homology

C;Keywords: alternative splicing; duplication; glycoprotein; immunoglobulin receptor; p

F;19-773/Product: signal sequence #status predicted <SIG>

F;19-575/Product: free secretory component #status predicted <MATW>

F;30-647/Domain: extracellular #status predicted <EXT>

F;39-117/Domain: immunoglobulin homology <IM1>

F;148-227/Domain: immunoglobulin homology <IM2>

F;253-326/Domain: immunoglobulin homology <IM3>

F;362-440/Domain: immunoglobulin homology <IM4>

F;471-540/Domain: immunoglobulin homology <IM5>

F;648-670/Domain: transmembrane #status predicted <TMW>

F;671-773/Domain: intracellular #status predicted <INT>

F;146-115,155-225,260-324,369-438,478-538/Disulfide bonds: #status predicted

F;108/Binding site: carbohydrate (Asn) (covalent) #status experimental

F;418/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match

Best Local Similarity 7.4%; Score 115; DB 1; Length 773;

Matches 53; Conservative 39; Mismatches 102; Indels 56; Gaps 11;

QY 45 EHSILAGDPFELEC--PVKYCANRPHVTWCKLNGT-TCVKLEDRQTSWKE----EKNISP 97



GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 8, 2006, 16:43:35 ; Search time 164 Seconds  
(without alignments)  
1243.279 Million cell updates/sec

Title: US-10-600-997-8  
Perfect score: 1557  
Sequence: 1 MKTLPMLTGKLFVWFLLI.....RLARNVKEAPTEYASICVRS 289

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000.

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1516	97.4	289	1 BTLA_HUMAN	Q7z6a9 homo sapien
2	713.5	45.8	306	1 BTLA_MOUSE	Q7tsa3 mus musculus
3	673.5	43.3	308	1 BTLA_RAT	Q6pm1 rattus norv
4	121.5	7.8	266	1 Q9CUC8_MOUSE	Q9cuc8 mus musculus
5	121.5	7.8	343	1 SLAP1_MOUSE	Q9qum4 mus musculus
6	121.5	7.8	343	2 Q544KI_MOUSE	Q15746 mus musculus
7	117	7.5	1914	1 MYLK_HUMAN	Q15746 homo sapien
8	116	7.5	1914	2 Q5MY99_HUMAN	Q5my99 homo sapien
9	116	7.5	1914	2 Q724J0_HUMAN	Q7z4j0 homo sapien
10	115	7.4	773	1 PIGR_RABIT	P01832 oryctolagus
11	115	7.4	841	2 P97484_MOUSE	P97484 mus musculus
12	113.5	7.3	841	2 Q8R2Z1_MOUSE	Q8r2z1 mus musculus
13	111	7.1	5992	2 Q5W615_CAEEL	Q5w615 caenorhabdi
14	111	7.1	6632	1 UNC89_CAEEL	Q01761 caenorhabdi
15	111	7.1	7122	2 Q5W616_CAEEL	Q5w616 caenorhabdi
16	111	7.1	7441	2 Q5W617_CAEEL	Q5w617 caenorhabdi
17	111	7.1	8081	2 Q72120_CAEEL	Q7z120 caenorhabdi
18	110	7.1	335	1 LIRN4_MOUSE	Q64281 mus musculus
19	109	7.0	1026	1 CBTN4_RAT	Q62845 rattus norv
20	107	6.9	1272	1 Q5GIT3_BRARE	Q5git3 brachydanio
21	107	6.9	1852	1 CACIS_CYPCA	P22316 cyprinus ca
22	106	6.8	410	2 Q6R3M2_BOMMO	Q6r3m2 bombyx mori
23	105.5	6.8	841	2 Q54999_MOUSE	Q54999 mus musculus
24	105	6.7	1272	2 Q4JDD5_BRARE	Q4jdd5 brachydanio
25	104.5	6.7	1036	1 CNTN2_CHICK	P28685 gallus gall
26	104.5	6.7	6875	2 Q28733_RABIT	Q28733 oryctolagus
27	104	6.7	410	2 Q6R3M0_BOMMO	Q6r3m0 bombyx mori
28	104	6.7	7562	2 Q10465_HUMAN	Q10465 homo sapien
29	104	6.7	34350	2 Q8WZ42_HUMAN	Q8wz42 homo sapien
30	103.5	6.6	1845	2 Q5MYA0_HUMAN	Q5mya0 homo sapien
31	102.5	6.6	5175	2 Q810L3_CAEEL	Q8i0l3 caenorhabdi

32	102.5	6.6	5198	2	Q76518_CAEEL	Q76518 caenorhabdi
33	102	6.6	326	2	Q8CAU4_MOUSE	Q8cau4 mus musculus
34	102	6.6	428	2	Q6F3J3_MOUSE	Q6f3j3 mus musculus
35	101.5	6.5	1029	2	Q6ZJ63_ORYSA	Q6zj63 oryza sativ
36	101.5	6.5	3410	2	Q7TN00_RAT	Q7tn00 rattus norv
37	101	6.5	5516	2	Q7Z248_BRARE	Q7z248 brachydanio
38	100.5	6.5	410	2	Q7YZA7_BOMMO	Q7yza7 bombyx mori
39	100.5	6.5	410	2	Q4FAT1_BOMMO	Q4fat1 bombyx mori
40	100.5	6.5	4071	2	Q6KDZ1_CHICK	Q6kdz1 gallus gall
41	100	6.4	1561	2	Q924D2_MOUSE	Q924d2 mus musculus
42	100	6.4	1949	2	Q6PDN3_MOUSE	Q6pdn3 mus musculus
43	99.5	6.4	26926	2	Q4UIZ6_HUMAN	Q4uiz6 homo sapien
44	99	6.4	1072	2	Q5VV43_HUMAN	Q5vv43 homo sapien
45	99	6.4	1109	2	Q9Y4G7_HUMAN	Q9y4g7 homo sapien

#### ALIGNMENTS

##### RESULT 1

ID	BTLA_HUMAN	STANDARD;	PRT;	289 AA.
AC	Q7Z6A9; Q6ZNH9;			
DT	13-SEP-2005 (Rel. 48, Created)			
DT	13-SEP-2005 (Rel. 48, Last sequence update)			
DT	13-SEP-2005 (Rel. 48, Last annotation update)			
DE	B and T lymphocyte attenuator precursor (B and T lymphocyte-associated protein).			
DE	Name=BTLLA;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;			
OC	Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE [MRNA], MUTAGENESIS OF TYR-226; TYR-257 AND TYR-282, N-GLYCOSYLATION, FUNCTION, AND INTERACTIONS WITH PTPN6 AND PTPN11.			
RX	PubMed=12796776; DOI=10.1038/nj1944;			
RA	Watanabe N., Gavrieli M., Sedy J.R., Yang J., Fallarino F., Loflin J.H., Hurchla M.A., Zimmerman N., Sim J., Zang X., Murphy T.L., Russell J.K., Allison J.P., Murphy K.M.;			
RA	"BTLLA is a lymphocyte inhibitory receptor with similarities to CTLA-4 and PD-1."			
RL	Nat. Immunol. 4:670-679(2003).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 4-289. TISSUE=Trachea;			
RC	PubMed=14702039; DOI=10.1038/ng1285;			
RA	Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R., Wakamatsu A., Hayashi K., Sato H., Negai K., Kimura K., Makita H., Sekine M., Ohyashi M., Nishi T., Shibahara T., Tanaka T., Ishii S., Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Omura Y., Abe K., Kamihara K., Kanda K., Yokoi T., Furuya T., Kikkawa E., Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K., Tanai H., Kimata M., Watanabe M., Hirakawa S., Chiba Y., Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S., Yoshioka Y., Matsunawa H., Ichihara T., Shiohata N., Sano S., Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O., Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H., Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B., Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y., Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T., Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,			

